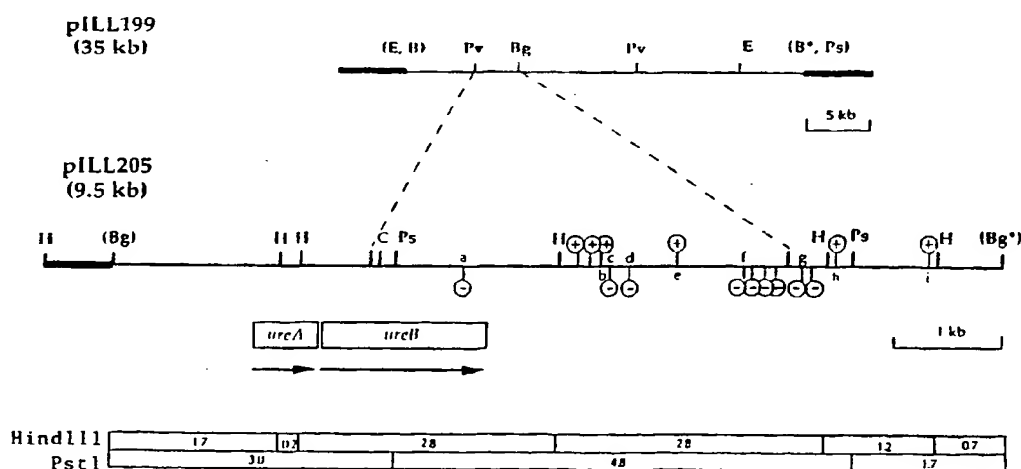




INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(51) International Patent Classification ⁵ : C12N 15/31, 9/80, C12Q 1/68, C12P 21/08, A61K 39/106, G01N 33/577		A1	(11) International Publication Number: WO 94/26901
(21) International Application Number: PCT/EP94/01625		(43) International Publication Date: 24 November 1994 (24.11.94)	
(22) International Filing Date: 19 May 1994 (19.05.94)		(74) Agents: GUTMANN, Ernest et al.; Ernest Gutmann-Yves Plasseraud S.A., 3, rue Chauveau-Lagarde, F-75008 Paris (FR).	
(30) Priority Data: 93401309.5 19 May 1993 (19.05.93) EP (34) Countries for which the regional or international application was filed: GB et al. PCT/EP93/03259 19 November 1993 (19.11.93) WO (34) Countries for which the regional or international application was filed: JP et al.		(81) Designated States: AU, CA, JP, KR, US, European patent (AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE).	
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(54) Title: IMMUNOGENIC COMPOSITIONS AGAINST HELICOBACTER INFECTION, POLYPEPTIDES FOR USE IN THE COMPOSITIONS AND NUCLEIC ACID SEQUENCES ENCODING SAID POLYPEPTIDES



(57) Abstract

The invention relates to an immunogenic composition, capable of inducing protective antibodies against *Helicobacter* infection, characterised in that it comprises: i) at least one sub-unit of a urease structural polypeptide from *Helicobacter pylori*, or a fragment thereof, said fragment being recognised by antibodies reacting with *Helicobacter felis* urease, and/or at least one sub-unit of a urease structural polypeptide from *Helicobacter felis*, or a fragment thereof, said fragment being recognised by antibodies reacting with *Helicobacter pylori* urease; ii) and/or, a Heat Shock protein (HSP), or chaperonin, from *Helicobacter*, or a fragment of said protein. The invention also relates to the preparation, by recombinant means, of such immunogenic compositions.

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IMMUNOGENIC COMPOSITIONS AGAINST HELICOBACTER
INFECTION, POLYPEPTIDES FOR USE IN THE COMPOSITIONS
AND NUCLEIC ACID SEQUENCES ENCODING SAID POLYPEPTIDES

The present invention relates to immunogenic compositions for inducing protective antibodies against Helicobacter spp. infection. It also relates to proteinaceous material derived from Helicobacter, and to nucleic acid sequences encoding them. Antibodies to these proteinaceous materials are also included in the invention.

H. pylori is a microorganism which infects human gastric mucosa and is associated with active chronic gastritis. It has been shown to be an aetiological agent in gastroduodenal ulceration (Peterson, 1991) and two recent studies have reported that persons infected with H. pylori had a higher risk of developing gastric cancer (Nomura et al, 1991 ; Parsonnet et al, 1991).

In vivo studies of the bacterium and, consequently, work on the development of appropriate preventive or therapeutic agents has been severely hindered by the fact that Helicobacter pylori only associates with gastric-type epithelium from very few animal hosts, none of which are suitable for use as laboratory models.

A mouse model of gastric colonisation has been developed using a helical bacterium isolated from cat gastric mucus (Lee et al, 1988, 1990) and identified as a member of the genus Helicobacter. It has been named H. felis (Paster et al, 1990).

To date, only limited information concerning H. felis and the extent of its similarities and

differences with H. pylori, is available. The reliability of the mouse model for the development of treatments for H. pylori infection is therefore uncertain. Recently, it was shown that H. pylori urease is a protective antigen in the H. felis / mouse model (Davin et al, 1993 ; Corthesy-Theulaz et al, 1993).

It is therefore an aim of the present invention to provide therapeutic and preventive compositions for use in Helicobacter infection, which furthermore can be tested in laboratory animals.

It is known that H. pylori expresses urease activity and that urease plays an important role in bacterial colonisation and mediation of certain pathogenic processes (Ferrero and Lee, 1991 ; Hazel et al, 1991).

The genes coding for the urease structural polypeptides of H. pylori (URE A, URE B) have been cloned and sequenced (Labigne et al, 1991 ; and French Patent Application FR 8813135), as have the genes coding the "accessory" polypeptides necessary for urease activity in H. pylori (International patent application WO 93/07273).

Attempts have been made to use nucleic acid sequences from the H. pylori urease gene cluster as probes to identify urease sequences in H. felis. However, none of these attempts have been successful. Furthermore, the establishment and maintenance of H. felis cultures in vitro is extremely difficult, and the large quantities of nucleases present in the bacteria complicates the extraction of DNA.

The present inventors have however, succeeded in cloning and sequencing the genes of the urease structural polypeptides of H. felis, and of the accessory polypeptides. This has enabled, in the

context of the invention, the comparison of the amino-acid sequence data for the H. felis ure gene products with that for Helicobacter pylori, and a high degree of conservation between the urease sub-units has been found. An immunological relationship between the 2 ureases exists, and protective antibodies to Helicobacter infection can be induced using the urease sub-units or fragments thereof as immunogens.

Indeed, to elucidate the efficiency of individual urease subunits to act as mucosal immunogens, the genes encoding the respective urease subunits (UreA and UreB) of Helicobacter pylori and Helicobacter felis have been cloned in an expression vector (pMAL), and expressed in Escherichia coli cells as translational fusion proteins. The recombinant UreA and UreB proteins have been purified by affinity and anion exchange chromatography techniques, and have predicted molecular weights of approximately 68 and 103 kDa, respectively. Western blotting studies indicated that the urease components of the fusion proteins are strongly immunogenic and are specifically recognized by polyclonal rabbit anti-Helicobacter sera. Orogastric immunization of mice with 50 μ g of recombinant H. felis UreB, administered in combination with a mucosal adjuvant (cholera toxin), protected 60 % (n = 7 ; p < 0.005) of mice from gastric colonization by H. felis bacteria at over 4 months. This compared with a value of 25 % (n = 8 ; p > 0.05) for the heterologous H. pylori UreB antigen. For the first time, a recombinant subunit antigen has been shown to induce an immunoprotective response against gastric Helicobacter infection.

The inventors have also identified, in the context of the invention, new Heat Shock Proteins or chaperonins, in Helicobacter, which have an enhancing

effect on urease activity. Use of the chaperonins in an immunogenic composition may induce therefore an enhancement of protection.

Indeed, the genes encoding each of the HspA and HspB polypeptides of Helicobacter pylori have been cloned, expressed independently as fused proteins to the Maltose-Binding-Protein (MBP), and purified on a large scale. These proteins have been used as recombinant antigens to immunize rabbits, and in Western immunoblotting assays as well as ELISA to determine their immunogenicity in patients infected with HP (HP+). The MBP-HspA and MBP-HspB fusion proteins have been shown to retain their antigenic properties. Comparison of the humoral immune response against HspA and/or HspB in (HP+) patient sera demonstrated that not only HspB but also HspA was recognized by (HP+) patient sera (29/38 and 15/38, respectively). None of the 14 uninfected patients had antibodies reacting with the Hsps.

The present invention concerns an immunogenic composition capable of inducing antibodies against Helicobacter infection characterised in that it comprises :

i) at least one sub-unit of a urease structural polypeptide from Helicobacter pylori, or a fragment thereof, said fragment being recognised by antibodies reacting with Helicobacter felis urease, and/or at least one sub-unit of a urease structural polypeptide from Helicobacter felis, or a fragment thereof, said fragment being recognised by antibodies reacting with Helicobacter pylori urease ;

ii) and/or a Heat Shock protein (HSP), or chaperonin, from Helicobacter, or a fragment of said protein.

Preferably, the immunogenic composition is capable of inducing protective antibodies.

According to a preferred embodiment, the immunogenic composition of the invention contains, as the major active ingredient, at least one sub-unit of a urease structural polypeptide from Helicobacter pylori and/or Helicobacter felis. The expression "urease structural polypeptide" signifies, in the context of the present invention, the enzyme of Helicobacter pylori or Helicobacter felis probably a major surface antigen composed of two repeating monomeric sub-units, a major sub-unit (product of the ure B gene) and a minor sub-unit, product of the ure A gene and which, when complemented by the presence of the products of the accessory genes of the urease gene cluster, are responsible for urease activity i.e. the hydrolysis of urea to liberate NH_4^+ in the two Helicobacter species. It is to be understood that in the absence of the accessory gene products, the urease structural polypeptides do not exhibit enzymatic activity, but are recognised by antibodies reacting with H. felis or H. pylori urease.

The term "immunogenic composition" signifies, in the context of the invention, a composition comprising a major active ingredient as defined above, together with any necessary ingredients to ensure or to optimise an immunogenic response, for example adjuvants, such as mucosal adjuvant, etc...

The Helicobacter pylori urease structural polypeptide has been described and sequenced by Labigne et al, 1991. The polypeptide described in this paper is particularly appropriate for use in the composition of the present invention. However, variants showing functional homology with this published sequence may be used, which comprise amino-

acid substitutions, deletions or insertions provided that the immunological characteristics of the polypeptide in so far as its cross-reactivity with anti-Helicobacter felis urease antibodies is concerned, are maintained. Generally speaking, the polypeptide variant will show a homology of at least 75% and preferably about 90% with the included sequence.

A fragment of the Helicobacter pylori urease structural polypeptide may also be used in the immunogenic composition of the invention, provided that the fragments are recognised by antibodies reacting with Helicobacter felis urease. Such a fragment will generally be comprised of at least 6 amino-acids, for example, from 6 to 100 amino-acids, preferably about 20-25. Advantageously, the fragment carries epitopes unique to Helicobacter.

Nucleic acid and amino-acid sequences may be interpreted in the context of the present invention by reference to figures 11 and 12, showing the genetic code and amino-acid abbreviations respectively.

The Helicobacter felis urease structural polypeptide suitable for use in the present invention is preferably that encoded by part of the plasmid pILL205 (deposited at the CNM on 25th August 1993, under number : CNM I-1355), and whose amino-acid sequence is shown in figure 3 (subunits A and B). Again, a variant of this polypeptide comprising amino-acid substitutions, deletions or insertions with respect to the figure 3 sequence may be used provided that the immunological cross-relationship with Helicobacter pylori urease is maintained. Such a variant normally exhibits at least 90 % homology or identity with the figure 3 sequence. An example of such variants are the urease A and B sub-units from

Helicobacter heilmannii (Solnick et al, 1994), shown to have 80 % and 92 % identity with the H. felis urease A and B sub-units, respectively.

Fragments of this urease or variants may be used in the immunogenic composition provided that the fragments are recognised by antibodies reacting with Helicobacter pylori urease. Again, the length of such a fragment is usually at least 6 amino-acids, for example from 6 to 100, preferably about 20 to 25. Preferably, the fragment carries epitopes unique to Helicobacter.

If variants or fragments of the native urease sequences are employed in the immunogenic composition of the invention, their cross-reactivity with antibodies reacting with urease from the other Helicobacter species can be tested by contacting the fragment or the variant with antibodies, preferably polyclonal raised to either the native or the recombinant urease or, alternatively, to whole Helicobacter. Preferably, the variants and fragments give rise to antibodies which are also capable of reacting with H. heilmannii urease. Cross protection to infection by H. heilmannii is therefore also obtained by the immunogenic composition of the invention.

The use of fragments of the urease structural genes is particularly preferred since the immunological properties of the whole polypeptide may be conserved whilst minimizing risk of toxicity.

The active component of the immunogenic composition of the invention may be comprised of one sub-unit only of the urease structural polypeptide, that is either sub-unit A or sub-unit B products of the ure A and ure B genes respectively. Compositions comprising only the urease sub-unit Ure B, of either

H. pylori or H. felis, or variants and fragments as defined above, are particularly advantageous. Most preferred are homologous systems wherein the urease sub-unit particularly sub-unit B, is derived from the organism against which protection is sought, e.g. H. felis sub-unit B against H. felis infection. However, the composition may contain both A and B sub-units, which are normally present as distinct polypeptides. However, it is possible, when the polypeptide is produced by recombinant means, to use a fusion protein comprising the entire sequences of the A and B gene products by the suppression of the stop-codon separating the two adjacent coding sequences.

The urease component of the immunogenic composition, whether sub-unit A or sub-unit B, may be used in the form of translational fusion proteins, for example with the Maltose-Binding-Protein (MBP). Other suitable fusions are exemplified in International Patent Application WO 90/11360. Another example of a suitable fusion protein is the "QIAexpress" system commercialised by QIAGEN, USA, which allows the 6xHis tag sequence to be placed at the 5' or 3' end of the protein coding sequence. The use of the active ingredients in the form of fusion proteins is however, entirely optional.

According to a further preferred embodiment, the immunogenic composition of the invention may comprise in addition to or instead of the urease structural polypeptide defined above, a Heat Shock Protein also known as a "chaperonin" from Helicobacter. These chaperonins have been elucidated by the inventors in the context of the present invention. Preferably, the chaperonin is from Helicobacter pylori. Such an HSP may be the urease-associated HSP A or HSP B or a mixture of the two, having the amino-acid sequence

illustrated in figure 6. These polypeptides are encoded by the plasmid pILL689 (deposited at CNCM on 25th August 1993, under number : CNCM I-1356). Particularly preferred is the H. pylori HSP-A protein, either alone or in combination with Hsp-B.

It is also possible to use, as HSP component, according to the invention, a polypeptide variant in which amino-acids of the figure 6 sequence have been replaced, inserted or deleted, the said variant normally exhibiting at least 75 %, and preferably at least 85 % homology with the native HSP. The variants preferably exhibit at least 75 %, for example at least 85 % identity with the native Hsp.

The variants may further exhibit functional homology with the native polypeptide. In the case of the HSP components, "functional homology" means the capacity to enhance urease activity in a micro-organism capable of expressing active urease, and/or the capacity to block infection by Helicobacter, particularly H. felis and H. pylori. The property of enhancing urease activity may be tested using the quantitative urease activity assay described below in the examples. Fragments of either or both of the HSP A and HSP B polypeptides preferably having at least 6 amino-acids, may be used in the composition. The fragments or variants of the HSP component used in the immunogenic composition of the invention are preferably capable of generating antibodies which block the urease enhancing effect normally exhibited by the HSPs. This property is also tested using the quantitative assay described in the examples. The presence of the chaperonins in the composition enhances the protection against Helicobacter pylori and felis.

The Hsp component of the immunogenic composition, whether HspA or HspB can be used in the form of a translational fusion protein, for example with the Maltose-Binding-Protein (MBP). As for the urease component, other suitable fusion partners are described in International Patent Application WO 90/11360. The "QIAexpress" system of QIAGEN, USA, may also be used. Again, the use of the proteins in the form of fusion proteins is entirely optional.

According to the invention therefore the immunogenic composition may comprise either a urease structural polypeptide as defined above, or a Helicobacter Hsp, particularly HspA or a combination of these immunogens.

According to a preferred embodiment, the immunogenic composition comprises, as urease component, both the A and B sub-units of both Helicobacter felis (i.e. without H. pylori urease) together with the HSP A and HSP B of Helicobacter pylori. Alternatively, the A and B sub-units of the Helicobacter felis urease may be used together with those of H. pylori, but without chaperonin component.

The immunological cross-reactivity between the ureases of the two different Helicobacter species enables the use of one urease only in the composition, preferably that of Helicobacter felis. The protective antibodies induced by the common epitopes will however be active against both Helicobacter pylori and Helicobacter felis. It is also possible that the composition induce protective antibodies to other species of Helicobacter, if the urease polypeptide or fragment carries epitopes occurring also on those other species.

The composition of the invention is advantageously used as an immunogenic composition or a

vaccine, together with physiologically acceptable excipients and carriers and, optionally, with adjuvants, haptens, carriers, stabilizers, etc. Suitable adjuvants include muranmyl dipeptide (MDP), complete and incomplete Freund's adjuvants (CFA and IFA) and alum. The vaccine compositions are normally formulated for oral administration.

The vaccines are preferably for use in man, but may also be administered in non-human animals, for example for veterinary purposes, or for use in laboratory animals such as mice, cats and dogs.

The immunogenic compositions injected into animals raises the synthesis in vivo of specific antibodies, which can be used for therapeutic purposes, for example in passive immunity.

The invention also relates to the proteinaceous materials used in the immunogenic composition and to proteinaceous material encoded by the urease gene clusters other than the A and B urease structural sub-units. "Proteinaceous material" means any molecule comprised of chains of amino-acids, eg. peptides, polypeptides or proteins, fusion or mixed proteins (i.e. an association of 2 or more proteinaceous materials, all or some of which may have immunogenic or immunomodulation properties), either purified or in a mixture with other proteinaceous or non-proteinaceous material. "Polypeptide" signifies a chain of amino-acids whatever its length and englobes the term "peptide". The term "fragment" means any amino-acid sequence shorter by at least one amino-acid than the parent sequence and comprising a length of amino-acids e.g. at least 6 residues, consecutive in the parent sequence.

The peptide sequences of the invention, may for example, be obtained by chemical synthesis, using a

technique such as the Merrifield technique and synthesiser of the type commercialised by Applied Biosystems.

In particular, the invention relates to proteinaceous material characterised in that it comprises at least one of the Helicobacter felis polypeptides encoded by the urease gene cluster of the plasmid pILL205 (CNCM I-1355), including the structural and accessory urease polypeptides, or a polypeptide having at least 90 % homology with said polypeptides, or a fragment thereof. Of particular interest are the gene products of the ure A and ure B genes, as illustrated in figure 3, or a variant thereof having at least 90 % homology or a fragment having at least 6 amino-acids. The fragments and the variants are recognised by antibodies reacting with Helicobacter pylori urease.

Amongst the polypeptides encoded by the accessory genes of the urease gene cluster, is the gene product of ure I, as illustrated in figure 9, which also forms part of the invention. Also included is a variant of the ure I product having at least 75 % homology, preferably at least 85 %, or a fragment of the gene product or of the variant having at least 6 amino-acids. The variant preferably has the capacity to activate the ure A and ure B gene products in the presence of the remaining urease accessory gene products. This functional homology can be detected by using the following test : 10^9 bacteria containing the ure I gene product variant are suspended in 1 ml of urea-indole medium and incubated at 37° C. The hydrolysis of the urea leads to the release of ammonium, which increases pH and induces a colour change from orange to fuscia-red. The observation of such a colour change demonstrates that the variant of

the ure I gene product under test is capable of activating the ure A and B gene products.

It is also possible that a fragment of the ure I gene product, if it has a length of, for example, at least 70 or 100 amino-acids, may also exhibit this functional homology with the entire polypeptide.

The fragments of ure I polypeptide or of the variant preferably are capable of inducing the formation of antibodies which block the urease maturation process. In other words, the fragments bear epitopes which play a decisive role in the interaction between the ure I and ure A / ure B gene products. .

The invention also relates to the proteinaceous material comprising at least one of the Heat Shock Proteins or chaperonins of Helicobacter pylori or a fragment thereof. Particularly preferred are the HSP A and HSP B polypeptides as illustrated in figure 6 or a polypeptide having at least 75 %, and preferably at least 80 or 90 %, homology or identity with the said polypeptide. A particularly preferred fragment of the Helicobacter pylori HSP A polypeptide is the C-terminal sequence :

G S C C H T G N H D H K H A K E H E A C C H D H K K H

or a sub-fragment of this sequence having at least 6 consecutive amino-acids. This C-terminal sequence is thought to act as a metal binding domain allowing binding of, for example, nickel.

The proteinaceous material of the invention may also comprise or consist of a fusion or mixed protein including at least one of the sub-units of the urease structural polypeptide of H. pylori and/or of H. felis, or fragments or variants thereof as defined above. Particularly preferred fusion proteins are the

Mal-E fusion proteins and QIAexpress system fusion proteins (QIAGEN, USA) as detailed above. The fusion or mixed protein may include, either instead of in addition to the urease sub-unit, a Heat Shock Protein, or fragment or variant thereof, as defined above.

The invention also relates to monoclonal or polyclonal antibodies to the proteinaceous materials described above. More particularly, the invention relates to antibodies or fragments thereof to any one of the Helicobacter felis polypeptides encoded by the urease gene cluster of the plasmid pILL205 (CNCM I-1355) including the structural and accessory urease polypeptides that is, structural genes ure A and ure B and the accessory genes known as ure C, ure D, ure E, ure F, ure G, ure H and ure I. The antibodies may also be directed to a polypeptide having at least 90 % homology with any of the above urease polypeptides or to a fragment thereof preferably having at least 6 amino-acids. The antibodies of the invention may specifically recognise Helicobacter felis polypeptides expressed by the urease gene cluster. In this case, the epitopes recognised by the antibodies are unique to Helicobacter felis. Alternatively, the antibodies may include or consist of antibodies directed to epitopes common to Helicobacter felis urease polypeptides and to Helicobacter pylori urease polypeptides. If the antibodies recognise the accessory gene products, it is particularly advantageous that they cross-react with the Helicobacter pylori accessory gene product. In this way, the antibodies may be used in therapeutic treatment of Helicobacter pylori infection in man, by blocking the urease maturation process.

Particularly preferred antibodies of the invention recognise the Helicobacter felis ure A

and/or ure B gene products, that is the A and B urease sub-units. Advantageously, these antibodies also cross-react with the Helicobacter pylori A and B urease sub-units, but do not cross-react with other ureolytic bacteria. Such antibodies may be prepared against epitopes unique to Helicobacter (see figure 4), or alternatively, against the whole polypeptides followed by screening out of any antibodies reacting with other ureolytic bacteria.

The invention also concerns monoclonal or polyclonal antibodies to the HSPs or fragments thereof, particularly to the HSP A and/or HSP B protein illustrated in figure 6. Polypeptides having at least 75 %, and preferably at least 80 %, or 90 % homology with the HSPs may also be used to induce antibody formation. These antibodies may be specific for the Helicobacter pylori chaperonins or, alternatively, they may cross-react with GroEL-like proteins or GroES-like proteins from bacteria other than Helicobacter, depending upon the epitopes recognised. Figure 7 shows the homologous regions of HSP A and HSP B with GroES-like proteins and GroEL-like proteins respectively from various bacteria. Particularly preferred antibodies are those specific for either the HSP A or HSP B chaperonins or those specifically recognising the HSP A C-terminal sequence having the metal binding function. Again, use of specific fragments for the induction of the antibodies ensures production of Helicobacter-specific antibodies.

The antibodies of the invention may be prepared using classical techniques. For example monoclonal antibodies may be produced by the hybridoma technique or by known techniques for the preparation of human antibodies, or by the technique described by Marks et

al (Journal of Molecular Biology, 1991, 222, p 581-597).

The invention also includes fragments of any of the above antibodies produced by enzyme digestion. Of particular interest are the Fab and F(ab')₂ fragments. Also of interest are the Facb fragments.

The invention also relates to purified antibodies or serum obtained by immunisation of an animal, e.g. a mammal, with the immunogenic composition, the proteinaceous material or fragment, or the fusion or mixed protein of the invention, followed by purification of the antibodies or serum. Also concerned is a reagent for the in vitro detection of H. pylori infection, containing at least these antibodies or serum, optionally with reagents for labelling the antibodies e.g. anti-antibodies etc.

The invention further relates to nucleic acid sequences coding for any of the above proteinaceous materials including peptides. In particular, the invention relates to a nucleic acid sequence characterised in that it comprises :

i) a sequence coding for the Helicobacter felis urease and accessory polypeptides as defined above, and a sequence coding for the HSP of H. pylori as defined above ;

or ii) a sequence complementary to sequence (i) ;

or iii) a sequence capable of hybridizing to sequence (i) or (ii) under stringent conditions ;

or iv) a fragment of any of sequences (i), (ii) or (iii) comprising at least 10 nucleotides.

Preferred nucleic acid sequences are those comprising all or part of the sequence of plasmid pIL205 (CNCM I-1355), for example the sequence of Figure 3, in particular that coding for the gene product of ure A and for ure B or the sequence of

Figure 9 (Ure I), or a sequence capable of hybridising with these sequences under stringent conditions, or a sequence complementary to these sequences, or a fragment comprising at least 10 consecutive nucleotides of these sequences.

Other preferred sequences are those comprising all or part of the sequence of plasmid pILL689 (CNCM I-1356), for example the sequence of figure 6, in particular that coding for HSP A and/or HSP B, or a sequence complementary to this sequence, or a sequence capable of hybridizing to this sequence under stringent conditions, or a fragment thereof.

High stringency hybridization conditions in the context of the invention are the following :

- 5 x SSC ;
- 50 % formamide at 37°C ;

or :

- 6 x SSC ;
- Denhard medium at 68°C.

The sequences of the invention also include those hybridizing to any of sequences (i), (ii) and (iii) defined above under non-stringent conditions, that is :

- 5 x SSC ;
- 0.1 % SDS ;
- 30 or 40 % formamide at 42°C, preferably 30 %.

The term "complementary sequences" in the context of the invention signifies "complementary" and "reverse" or "inverse" sequences.

The nucleic acid sequences may be DNA or RNA.

The sequences of the invention may be used as nucleotide probes in association with appropriate labelling means. Such means include radio-active isotopes, enzymes, chemical or chemico-luminescent markers, fluoro-chromes, haptens, or antibodies. The

markers may optionally be fixed to a solid support, for example a membrane, or particles.

As a preferred marker, radio-active phosphorous (^{32}P) is incorporated at the 5'-end of the probe sequence. The probes of the invention comprise any fragment of the described nucleic acid sequences and may have a length for example of at least 45 nucleotides, for example 60, 80 or 100 nucleotides or more. Preferred probes are those derived from the ure A, ure B, ure I, HSP A and HSP B genes.

The probes of the invention may be used in the in vitro detection of Helicobacter infection in a biological sample, optionally after a gene amplification reaction. Most advantageously, the probes are used to detect Helicobacter felis or Helicobacter pylori, or both, depending on whether the sequence chosen as the probe is specific to one or the other, or whether it can hybridise to both. Generally, the hybridisation conditions are stringent in carrying out such a detection.

The invention also relates to a kit for the in vitro detection of Helicobacter infection, characterised in that it comprises :

- a nucleotide probe according to the invention, as defined above ;
- an appropriate medium for carrying out a hybridisation reaction between the nucleic acid of Helicobacter and the probe ;
- reagents for the detection of any hybrids formed.

The nucleotide sequences of the invention may also serve as primers in a nucleic acid amplification reaction. The primers normally comprise at least 10 consecutive nucleotides of the sequences described above and preferably at least 18. Typical lengths are

from 25 to 30 and may be as high as 100 or more consecutive nucleotides. Such primers are used in pairs and are chosen to hybridize with the 5' and 3'-ends of the fragment to be amplified. Such an amplification reaction may be performed using for example the PCR technique (European patent applications EP200363, 201184 and 229701). The Q- β -replicase technique (Biotechnology, vol. 6, Oct. 1988) may also be used in the amplification reaction.

The invention also relates to expression vectors characterised in that they contain any of the nucleic acid sequences of the invention. Particularly preferred expression vectors are plasmids pILL689 and pILL205 (CNCM I-1356 and CNCM I-1355, respectively). The expression vectors will normally contain suitable promoters, terminators and marker genes, and any other regulatory signals necessary for efficient expression.

The invention further relates to prokaryotic or eukaryotic host cells stably transformed by the nucleic acid sequences of the invention. As examples of hosts, mention may be made of higher eukaryotes such as CHO cells and cell-lines ; yeast, prokaryotes including bacteria such as E. coli e.g. E. coli HB 101 ; Mycobacterium tuberculosis ; viruses including baculovirus and vaccinia. Usually the host cells will be transformed by vectors. However, it is also possible within the context of the invention, to insert the nucleic acid sequences by homologous recombination, using conventional techniques.

By culturing the stably transformed hosts of the invention, the Helicobacter urease polypeptide material and, where applicable, the HSP material can be produced by recombinant means. The recombinant proteinaceous materials are then collected and purified. Pharmaceutical compositions are prepared by

combining the recombinant materials with suitable excipients, adjuvants and optionally, any other additives such as stabilizers.

The invention also relates to plasmids pILL920 (deposited at CNCM on 20.07.1993, under accession number I-1337) and pILL927 (CNCM I-1340, deposited on 20.07.1993) constructed as described in the examples below.

Different aspects of the invention are illustrated in the figures :

Figure 1 :

Transposon mutagenesis and sequencing of pILL205. Linear restriction maps of recombinant cosmid pILL199 and recombinant plasmid pILL205 (and the respective scale markers) are presented. Numbers in parentheses indicate the sizes of H.felis DNA fragments inserted into one of the cloning vectors (pILL575 or pILL570, respectively). The "plus" and "minus" signs within circles correspond to the insertion sites of the MiniTn3-Km transposon in pILL205 ; "plus" signs indicate that the transposon did not inactivate urease expression, whereas negative signs indicate that urease expression was abolished. The letters refer to mutant clones which were further characterised for quantitative urease activity and for the synthesis of urease gene products. The location of the structural urease genes (ure A and ure B) on pILL205 are represented by boxes, the lengths of which are proportional to the sizes of the respective open-reading frames. The arrows refer to the orientation of transcription. The scale at the bottom of the figure indicates the sizes (in kilobases) of the HindIII and PstI restriction fragments. Restriction sites are

represented as follows : B, BamHI ; Pv, PvuII ; Bg, BglII ; E, EcoRI ; H, HindIII ; C, ClaI ; Ps, PstI. Letters within parentheses indicate that the sites originated from the cloning vector.

Figure 2 :

Western blot analysis of whole-cell extracts of E. coli HB101 cells harbouring recombinant plasmids were reacted with rabbit polyclonal antiserum (diluted 1:1, 1000) raised against H. felis bacteria. A) extracts were of E. coli cells harbouring : plasmid vector pILL570 (lane 1) ; recombinant plasmid pILL205 (lane 2) ; and pILL205 derivative plasmids disrupted in loci "a", "b", "c", "d", and "e" (lanes 3-7). B) Extracts were of E. coli cells harbouring : recombinant plasmid pILL753 containing the H. pylori ure A and ure B genes (Labigne et al., 1991) (lane 1) ; and pILL205 derivative plasmids disrupted in loci "f", "g", "h", and "i" (lanes 2-5). The small arrow heads indicate polypeptides of approximately 30 and 66 kilodaltons which represent putative Ure A and Ure B gene products of H. felis. The large arrow heads in panel B indicate the corresponding gene products of H. pylori which cros-reacted with the anti-H. felis serum. The numbers indicate the molecular weights (in thousands) of the protein standards.

Figure 3 :

Nucleotide sequence of the H. felis structural urease genes. Numbers above the sequence indicate the nucleotide positions as well as the amino acid position in each of the two Ure A and Ure B polypeptides. Predicted amino acid sequences for Ure A (bp 43 to 753) and Ure B (766 to 2616) are shown below

the sequence. The putative ribosome-binding site (Shine-Dalgarno sequence, SD) is underlined.

Figure 4 :

Comparison of sequences for the structural urease genes of H. felis to : a) the sequence of the two subunits of H. pylori urease (Labigne et al., 1991) ; b) the sequence of the three subunits of Proteus mirabilis urease (Jones and Mobley, 1989) ; c) the sequence of the single subunit of jack bean urease. Gaps (shown by dashes) have been introduced to ensure the best alignment. *, amino acids identical to those of the H. felis sequence ; =, amino-acids shared by the various ureases ; ., amino-acids unique to the Helicobacter ureases. The percentages relate to the number of amino acids that are identical to those of the H. felis urease subunits. H.f., Helicobacter felis ; H.p., Helicobacter pylori ; P.m., Proteus mirabilis ; J.b., Jack bean.

Figure 5 :

Restriction map of the recombinant plasmids pILL689, pILL685, and pILL691. The construction of these plasmids is described in details in Table 1. Km within triangles depicts the site of insertion of the kanamycin cassette which led to the construction of plasmids pILL687, pILL688 and pILL696 (table 2). Boxes underneath the maps indicate the position of the three genetic elements deduced from the nucleotide sequence, namely IS5, Hsp A and Hsp B.

Figure 6 :

Nucleotide sequence of the Helicobacter pylori Heat Shock Protein gene cluster. The first number above the sequence indicates the nucleotide positions, whereas the second one numbers the amino-acid residue

position for each of the Hsp A and Hsp B protein. The putative ribosome-binding sequences (Shine- Dalgarno [SD] sites) are underlined.

Figure 7 :

Comparison of the deduced amino-acid sequence of Helicobacter pylori Hsp A (A) or Hsp B (B) with that of other GroEL-like (A) or GroES-like (B) proteins. Asteriks mark amino-acids identical with those in the Helicobacter pylori Hsp A or Hsp B sequences.

Figure 8 :

Expression of the Helicobacter pylori Hsp A Heat-Shock proteins in E. coli minicells. The protein bands with apparent molecular masses of 58 and 13 kDA, corresponding to the Helicobacter pylori Hsp A and Hsp B Heat-Shock Proteins are clearly visible in the lanes corresponding to plasmids pILL689 and pILL692 and absent in the vector controls (pILL570 and pACYC177, respectively)

Figure 9 :

Nucleotide sequence of the Helicobacter felis ure I gene and deduced amino-acid sequence.

Figure 10 :

Comparison of the amino-acid sequence of the ure I proteins deduced from the nucleotide sequence of the ure I gene of Helicobacter felis and that of Helicobacter pylori.

Figure 11 :

Genetic code. Chain-terminating, or "nonsense", codons. Also used to specify the initiator formyl-Met-tRNA^{Met}_f. The Val triplet GUG is therefore

"ambiguous" in that it codes both valine and methionine.

Figure 12 :

Signification of the one-letter and three-letter amino-acid abbreviations.

Figure 13 :

Purification of H. pylori UreA-MBP recombinant protein using the pMAL expression vector system. Extracts from the various stages of protein purification were migrated on a 10 % resolving SDS-polyacrylamide gel. Following electrophoresis, the gel was stained with Coomassie blue. The extracts were : 1) non-induced cells ; 2) IPTG-induced cells ; French press lysate of induced cell extract ; 5) eluate from amylose resin column ; 6) eluate from anion exchange column (first passage) ; 7) eluate from anion exchange column (second passage) ; 8) SDS-PAGE standard marker proteins.

Figure 14 :

Recognition of UreA recombinant fusion proteins by polyclonal rabbit anti-Helicobacter sera. Protein extracts of maltose-binding protein (MBP, lane 1), H. felis UreA-MBP (lane 2), and H. pylori UreA-MBP (lane 3) were Western Blotted using rabbit polyclonal antisera (diluted 1 : 5000) raised against whole-cell extracts of H. pylori and H. felis. The purified fusion proteins are indicated by an arrow. Putative degradation products of the proteins are shown by an asterisk.

Figure 15 :

Recognition of UreB recombinant fusion proteins by rabbit antisera raised against purified homologous

and heterologous UreB' proteins. Nitrocellulose membranes were blotted with the following extracts : 1) standard protein markers ; 2) H. felis UreA-MBP ; 3) MBP ; 4) H. pylori UreA-MBP. The membranes were reacted with polyclonal rabbit antisera (diluted 1 : 5000) raised against MBP-fused H. pylori and H. felis Ure B sub-units, respectively. The molecular weights of standard proteins are presented on the left-hand side of the blots.

Figure 16 :

Western blot analysis of H. pylori and H. felis whole-cell extracts with antisera raised against purified UreB MBP-fused recombinant proteins. SDS-PAGE whole extracts of H. Felis (lane 1) and H. pylori (lane 2) cells were reacted with polyclonal rabbit antisera raised against purified H. pylori UreB and H. felis UreB MBP-fused proteins (sera diluted 1 : 5000). The difference in gel mobility of the respective non-recombinant UreB sub-units of H. felis and H. pylori can be seen. The numbers on the left refer to the molecular weights of standard marker proteins.

Figure 17 :

SDS-PAGE analysis of material eluted from the amylose column (lanes 2 and 3) or from the Ni-NTA column following elution : with buffer E (pH 4.5), lanes 4 and 5 ; or buffer C (pH 6.3), lanes 6 and 7. Material eluted from a lysate of MC1061 (PILL933) (lanes 2, 3, 5 and 7) and material eluted from a lysate of MC1061 (PMAL-c2) (lanes 4 and 6). Lane 3 contains the same material as in lane 2 except that it was resuspended in buffer E, thus demonstrating that buffer E is responsible for dimer formation of the MBP-HspA subunit, as seen in lanes 3 and 5.

Figure 18 :

Serum IgG responses to MBP (bottom), MBP-HspA (top) and MBP-HspB (middle) of 28 H. pylori infected patients (squares, left) and 12 uninfected patients (circles, right). The optical density of each serum in the ELISA assay described in Experimental procedures was read at 492 nm, after a 30 mn incubation. The sizes of the symbols are proportional to the number of sera giving the same optical density value.

EXAMPLES**I - CLONING, EXPRESSION AND SEQUENCING OF H. FELIS UREASE GENE :****EXPERIMENTAL PROCEDURES FOR PART I :****Bacterial strains and culture conditions :**

H. felis (ATCC 49179) was grown on blood agar base no. 2 (Oxoid) supplemented with 5 % (v/v) lysed horse blood (BioMerieux) and an antibiotic supplement consisting of 10 ng ml⁻¹ vancomycin (Lederle Laboratories), 2.5 µg ml⁻¹ polymyxin B (Pfizer), 5µg ml⁻¹ trimethoprim (Sigma Chemical Co.) and 2.5 µg ml⁻¹ amphotericin B (E.R Squibb and Sons, Inc.). Bacteria were cultured on freshly prepared agar plates and incubated, lid uppermost, under microaerobic conditions at 37°C for 2-3 days. E. coli strains HB101 (Boyer and Roulland-Dussoix, 1969) and MC1061 (Maniatis et al., 1983), used in the cloning experiments, were grown routinely in Luria broth without glucose added or on Luria agar medium, at 37°C. Bacteria grown under nitrogen-limiting

conditions were passaged on a nitrogen-limiting solid medium consisting of ammonium-free M9 minimal medium (pH 7.4) supplemented with 0.4 % (w/v) D-glucose and 10 mM L-arginine (Cussac et al., 1992).

DNA manipulations :

All standard DNA manipulations and analyses, unless mentioned otherwise, were performed according to the procedures described by Maniatis et al. (1983).

Isolation of *H. felis* DNA :

Total genomic DNA was extracted by an sarkosyl-proteinase K lysis procedure (Labigne-Roussel et al., 1988). Twelve blood agar plates inoculated with *H. felis* were incubated in an anaerobic jar (BBL) with an anaerobic gaspak (BBL 70304) without catalyst, for 1-2 days at 37°C. The plates were harvested in 50 ml of a 15 % (v/v) glycerol - 9 % (w/v) sucrose solution and centrifuged at 5,000 rpm (in a Sorvall centrifuge), for 30 min at 4°C. The pellet was resuspended in 0.2 ml 50 mM D-glucose in 25 mM Tris-10 mM EDTA (pH 8.0) containing 5 mg ml⁻¹ lysozyme and transferred to a VTI65 polyallomer quick seal tube. A 0.2 ml aliquot of 20 mg ml⁻¹ proteinase K and 0.02 ml of 5M sodium perchlorate were added to the suspension. Cells were lysed by adding 0.65 ml of 0.5M EDTA -10 % (w/v) Sarkosyl, and incubated at 65°C until the suspension cleared (approximately 5 min). The volume of the tube was completed with a CsCl solution consisting (per 100 ml) of 126 g CsCl, 1 ml aprotinine, 99 ml TES buffer (30 mM Tris, 5 mM EDTA, 50 mM NaCl (pH 7.5). Lysates were centrifuged at 45 000 rpm, for 15-18 h at 18°C. Total DNA was collected and dialysed against TE buffer (10 mM Tris, 1 mM EDTA), at 4°C.

Cosmid cloning :

Chromosomal DNA from H. felis was cloned into cosmid vector pILL575, as previously described (Labigne et al, 1991). Briefly, DNA fragments arising from a partial digestion with Sau3A were sized on a (10 to 40 %) sucrose density gradient and then ligated into a BamHI-digested and dephosphorylated pILL575 DNA preparation. Cosmids were packaged into phage lambda particles (Amersham, In Vitro packaging kit) and used to infect E. coli HB101. To screen for urease expression, kanamycin-resistant transductants were replica-plated onto solid nitrogen-mimicking medium (see above) containing (20 $\mu\text{g ml}^{-1}$) kanamycin that had been dispensed into individual wells of microtitre plates (Becton Dickinson). The microtitre plates were incubated aerobically, at 37°C for 2 days before adding 0.1 ml urease reagent (Hazell et al., 1987) to each of the wells. Ureolysis was detected within 5-6 h at 37°C by a colour change in the reagent. Several urease-positive cosmid clones were restriction mapped and one was selected for subcloning.

Subcloning of H. felis DNA :

A large-scale CsCl plasmid preparation of cosmid DNA was partially digested Sau3A. DNA fragments (7 - 11 kb) were electroeluted from an agarose gel and purified using phenol-chloroform extractions. Following precipitation in cold ethanol, the fragments were ligated into Bg/III-digested plasmid pILL570 (Labigne et al., 1991) and the recombinant plasmids used to transform competent E. coli MC1061 cells. Spectinomycin-resistant transformants were selected and screened for urease expression under nitrogen-rich (Luria agar) and nitrogen-limiting conditions.

Quantitative urase activity :

Cultures grown aerobically for 2.5 days at 37°C were harvested and washed twice in 0.85 % (w/v) NaCl. Pellets were resuspended in PEB buffer (0.1 M sodium phosphate buffer (pH 7.4) containing 0.01 M EDTA) and then sonicated by four 30-sec bursts using a Branson Sonifier model 450 set at 30 W, 50 % cycle. Cell debris was removed from the sonicates by centrifugation. Urease activities of the sonicates were measured in a 0.05 M urea solution prepared in PEB by a modification of the Berthelot reaction (Cussac et al., 1992). Urease activity was expressed as $\mu\text{mol urea min}^{-1}\text{mg}^{-1}$ bacterial protein.

Protein determination :

Protein concentrations were estimated with a commercial version of the bradford assay (Sigma Chemicals).

Transposon mutagenesis :

Random insertional mutations were generated within cloned *H. felis* via a MiniTn3-Km delivery system (Labigne et al., 1992). In brief, *E. coli* HB101 cells containing the transposase-encoding plasmid pTCA were transformed with plasmid pILL570 containing cloned *H. felis* DNA. Transposition of the MiniTn3-Km element into the pILL570 derivative plasmids was effected via conjugation. The resulting cointegrates were then selected for resolved structures in the presence of high concentrations of kanamycin (500 mg l^{-1}) and spectinomycin (300 mg l^{-1}).

SDS-PAGE and Western blotting :

Solubilised cell extracts were analysed on slab gels, comprising a 4.5 % acrylamide stacking gel and 12.5 % resolving gel, according to the procedure of

Laemmli (Laemmli, 1970). Electrophoresis was performed at 200V on a mini-slab gel apparatus (Bio-Rad).

Proteins were transferred to nitrocellulose paper (Towbin et al., 1979) in a Mini Trans-Blot transfer cell (Bio-Rad) set at 100 V for 1 h (with cooling). Nitrocellulose membranes were blocked with 5 % (w/v) purified casein (BDH) in phosphate-buffered saline (PBS, pH 7.4) at room temperature, for 2 h (Ferrero et al., 1992). Membranes were reacted at 4°C overnight with antisera diluted in 1 % (w/v) casein prepared in PBS. Immunoreactants were then detected using a biotinylated secondary antibody (Kirkegaard and Perry Lab.) in combination with avidin-peroxidase (KPL). A substrate solution composed of 0.3 % (w/v) 4-chloro-1-naphthol (Bio-rad) was used to visualise reaction products.

DNA Sequencing :

DNA fragments to be sequenced were cloned into M13mp18 and M13mp19 (Meissing and Vieira, 1982) bacteriophage vectors (Pharmacia). Competent E. coli JM101 cells were transfected with recombinant phage DNA and plated on media containing X-gal (5-bromo-4-chloro-3-indolyl- β -D-galactopyranoside) and isopropyl- β -D-thiogalactopyranoside. Plaques arising from bacteria infected with recombinant phage DNA were selected for the preparation of single-stranded DNA templates by polyethylene glycol treatment (Sanger et al., 1977). Single-stranded DNA sequenced according to the dideoxynucleotide chain termination method using a Sequenase kit (United States Biochemical Corp.).

Nucleotide sequence accession number :

The nucleotide accession number is X69080 (EMBL Data Library).

RESULTS OF PART I EXPERIMENTS :**Expression of urease activity by *H. felis* cosmid clones :**

Cloning of partially digested fragments (30 to 45 kb in size) of *H. felis* chromosomal DNA into the cosmid vector pILL575 resulted in the isolation of approximately 700 cosmid clones. The clones were subcultured on nitrogen-limiting medium in order to induce urease expression (Cussac et al., 1992). Six of these were identified as being urease-positive after 5-6 h incubation (as described in the Experimental procedures section). No other urease-positive cosmid clones were identified, even after a further overnight incubation. Restriction enzyme analysis of 3 clones harbouring the urease-encoding cosmids revealed a common 28 kd DNA fragment. A cosmid (designated pILL199) containing DNA regions at both extremities of the common fragment was selected for subcloning.

Identification of *H. felis* genes required for urease expression when cloned in *E. coli* cells :

To define the minimum DNA region necessary for urease expression in *E. coli* cells, the urease-encoding cosmid pILL199 was partially digested with Sau3A and the fragments were subcloned into plasmid pILL570. The transformants were subcultured on nitrogen-rich and nitrogen-limiting media and screened for an urease-positive phenotype. Five transformants expressed urease activity when grown under nitrogen-limiting conditions, whereas no activity was detected following growth on nitrogen-rich medium. Restriction mapping analyses indicated that the urease-encoding plasmids contained inserts of between 7 and 11 kb. The

plasmid designated pILL205 was chosen for further studies.

Random mutagenesis of cloned H. felis DNA was performed to investigate putative regions essential for urease expression in E. coli and to localise the region of cloned DNA that contained the structural urease genes. Random insertion mutants of the prototype plasmid pILL205 were thus generated using the MiniTn3-Km element (Labigne et al, 1992). The site of insertion was restriction mapped for each of the mutated copies of pILL205 and cells harbouring these plasmids were assessed qualitatively for urease activity (figure 1). A selection of E. coli HB101 cells harbouring the mutated derivatives of pILL205 (designated "a" to "i") were then used both for quantitative urease activity determinations, as well as for the detection of the putative urease subunits by Western blotting.

The urease activity of E. coli HB101 cells harbouring pILL205 was $1.2 \pm 0.5 \mu\text{mol urea min}^{-1}\text{mg}^{-1}$ bacterial protein (table 1), which is approximately a fifth that of the parent H. felis strain used for the cloning. Insertion of the transposon at sites "a", "c", "d", "f" and "g" resulted in a negative phenotype, whilst mutations at sites "b", "e", "h" and "i" had no significant effect on the urease activities of clones harbouring these mutated copies of pILL205 (table 1). Thus mutagenesis of pILL205 with the MiniTn3-Km element identified three domains as being required for H. felis urease gene expression in E. coli cells.

Localisation of the H. felis urease structural genes :

Western blot analysis of extracts of E. coli cells harbouring pILL205 indicated the presence of two

polypeptides of approximately 30 and 66 kDa which cross-reacted with polyclonal H. felis rabbit antiserum (Figure 2A). These proteins were not produced by bacteria carrying the vector (pILL570). Native H. felis urease has been reported to be composed of repeating monomeric subunits with calculated molecular weights of 30 and 69 kDa (Turbett et al, 1992). Thus the 30 and 66 kDa proteins were thought to correspond to the ure A and ure B gene products, respectively. Interestingly an extract of E. coli cells harbouring the recombinant plasmid pILL763 (Cussac et al, 1992) containing the Helicobacter pylori ure A and ure B genes, expressed two polypeptides with approximate molecular sizes of 30 and 62 kDa which cross-reacted with the anti-H. felis antisera (figure 2B).

Table 1. Mutagenesis of *E. coli* clones and effect on urease activity.

plasmids ^a	Urease activity ^b ($\mu\text{mol urea min}^{-1} \text{mg}^{-1} \text{protein}$)
pILL205	1.2 ± 0.46 ^c
pILL205 :: a	neg ^d
pILL205 :: b	0.74 ± 0.32
pILL205 :: c	neg
pILL205 :: d	neg
pILL205 :: e	0.54 ± 0.15
pILL205 :: f	neg
pILL205 :: g	neg
pILL205 :: h	1.05 ± 0.25
pILL205 :: i	0.93 ± 0.35

^a *E. coli* cells harboured pILL205 and its derivatives constructed by transposon mutagenesis. The letters correspond to the insertion sites of the MiniTn3-transposon on pILL205.

^b Activities of bacteria grown aerobically for 3 days at 37 °C on solid M9 minimal medium supplemented with 10 mM L-arginine. The values represent the means \pm standard deviations calculated from three determinations.

^c Urease activity was approximately a fifth as large as that of *H. felis* wild-type strain (ATCC 49179) i.e. $5.7 \pm 0.1 \mu\text{mol urea min}^{-1} \text{mg}^{-1} \text{protein}$ (Ferrero and Lee, 1991).

^d No activity detected (limit of detection was $< 1 \text{ nmol urea min}^{-1} \text{mg}^{-1}$ of bacterial protein).

Clones harbouring the mutated derivatives of pILL205, in all but one case, expressed the ure A and ure B gene products (Figures 2A, B). Given that several of the mutants (i.e. mutants "c", "d", "f" and "g") synthesised the urease subunits yet did not produce an active enzyme, it is possible to speculate that accessory functions essential for urease activity may have been disrupted by transposon insertion. In contrast, the mutant designated pILL205::a did not produce the ure B product and was urease-negative. Thus the site of transposon insertion was presumed to be located in the ure B gene. Sequence analyses of the DNA region corresponding to insertion site "a" were undertaken to elucidate potential open reading frames encoding the structural polypeptides of H. felis urease.

Sequence analyses of H. felis structural urease genes :

Sequencing of a 2.4 kb region of H. felis DNA adjacent to transposon insertion site "a" resulted in the identification of two open reading frames (ORFs) designated ure A and ure B which are transcribed in the same direction (figure 3). The transposon was confirmed to be located at 240 bp upstream from the end of ure B. Both ORFs commenced with an ATG start codon and were preceded by a site similar to the E. coli consensus ribosome-binding sequence (Shine and Dalgarno, 1974). The intergenic space for the H. felis structural genes consisted of three codons which were in phase with the adjacent open-reading frames. This suggests that, as has already been observed to be the case for Helicobacter pylori (Labigne et al, 1991), a single mutation in the stop codon of the ure A gene

would theoretically result in a fused single polypeptide.

The H. felis ure A and ure B genes encode polypeptides with calculated molecular weights of 26 074 kA and 61 663 Da, respectively, which are highly homologous at the amino-acid sequence level to the ure A and ure B gene products of H. pylori. The levels of identity between the corresponding ure A and ure B gene products of the two Helicobacter spp. was calculated to be 73.5 % and 88.2 % respectively. From the amino-acid sequence information, the predicted molecular weights of the ure A and ure B polypeptides from H. felis and H. pylori (Labigne et al, 1991) are very similar. Nevertheless the ure B product of H. felis had a lower mobility than the corresponding gene product from Helicobacter pylori when subjected to SDS-polyacrylamide gel electrophoresis (figure 2B)

II - EXPRESSION OF RECOMBINANT UREASE SUBUNIT PROTEINS FROM H. PYLORI AND H. FELIS : ASSESSMENT OF THESE PROTEINS AS POTENTIAL MUCOSAL IMMUNOGENS IN A MOUSE MODEL :

The aims of the study were to develop recombinant antigens derived from the urease subunits of H. pylori and H. felis, and to assess the immunoprotective efficacies of these antigens in the H. felis/mouse model. Each of the structural genes encoding the respective urease subunits from H. pylori and H. felis was independently cloned and over-expressed in Escherichia coli. The resulting recombinant urease antigens (which were fused to a 42 kDa maltose-binding protein of E. coli) were purified in large quantities from E. coli cultures and were immunogenic, yet enzymatically inactive. The findings demonstrated the

feasibility of developing a recombinant vaccine against H. pylori infection.

EXPERIMENTAL PROCEDURES FOR PART II :

Bacterial strains, plasmids and growth conditions :

H. felis (ATCC 49179) was grown on a blood agar medium containing blood agar base no. 2 (Oxoid) supplemented with 10% lysed horse blood (BioMérieux) and an antibiotic supplement consisting of vancomycin (10 µg/mL), polymyxin B (25 ng/mL), trimethoprim (5 µg/mL) and amphotericin B (2.5 µg/mL). Bacteria were cultured under microaerobic conditions at 37° C for 2 days, as described previously. E. coli strains MC1061 and JM101, used in cloning and expression experiments, were grown routinely at 37° C in Luria medium, with or without agar added. The antibiotics carbenicillin (100 µg/mL) and spectinomycin (100 µg/mL) were added as required.

DNA manipulations and analysis :

All DNA manipulations and analyses, unless mentioned otherwise, were performed according to standard procedures. Restriction and modification enzymes were purchased from Amersham (France). DNA fragments to be cloned were electroeluted from agarose gels and then purified by passage on Elutip mini-columns (Schleicher and Schull, Germany). Single-stranded DNA sequencing was performed using M13mp18 and M13mp19 bacteriophage vectors (Pharmacia, France). Single-stranded DNA templates were prepared from recombinant phage DNA by polyethylene glycol treatment. Sequencing of the templates was achieved according to the dideoxynucleotide chain termination

method using a Sequenase kit (United States Biochemical Corp., U.S.A.).

Preparation of inserts for cloning using the polymerase chain reaction (PCR) :

To clone the ureA genes of H. pylori and H. felis, degenerated 36-mer primers were conceived from the published urease sequences (Labigne et al., 1991 ; Ferrero and Labigne, 1993) (primer set #1 ; refer to table 2). Purified DNA from E. coli clones harbouring plasmids pILL763 and pILL207 (table 3), that encoded the structural genes of H. pylori and H. felis ureases, were used as template material in PCR reactions. Reaction samples contained : 10 - 50 ng of denatured DNA ; PCR buffer (50 mmol/L KCl in 10 mmol/L Tris-HCl [pH 8.3]) ; dATP, dGTP, dCTP and dTTP (each at a final concentration of 1.25 mmol/L) ; 2.5 mmol/L MgCl₂ ; 25 pmol of each primer and 0.5 μ L Tag polymerase. The samples were subjected to 30 cycles of the following programme : 2 min at 94° C, 1 min at 40° C.

The amplification products were cloned into the cohesive ends of the pAMP vector (figure 1) according to the protocol described by the manufacturer ("CloneAmp System", Gibco BRL ; Cergy Pontoise, France). Briefly, 60 ng of amplification product was directly mixed in a buffer (consisting of 50 mmol/L KCl, 1.5 mmol/L MgCl₂, 0.1 % (wt/vol) gelatine in 10 mmol/L Tris-HCl, pH 8.3) with 50 ng of the pAMP 1 vector DNA and 1 unit of uracil DNA glycosylase. Ligation was performed for 30 min at 37° C. Competent cells (200 μ L) of E. coli MC1061 were transformed with 20 μ L of the ligation mixture. Inserts were subsequently excised from the polylinker of the pAMP vector by double digestion with BamH1 and Pst1, and

then subcloned into the expression vector pMAL (New England Biolabs Inc., Beverly, USA) chosen for the production of recombinant antigens (pILL919 and pILL920, respectively, figure 13), as well as in M13mp bacteriophage for sequencing.

Amplification of a product containing the ureB gene of H. pylori was obtained by PCR using a couple of 35-mer primers (set #2, table 2). The PCR reaction mixtures were first denatured for 3 min at 94° C, then subjected to 30 cycles of the following programme : 1 min at 94° C, 1 min at 55° C and 2 min at 72° C. The purified amplification product (1850 bp) was digested with EcoRI and PstI and then cloned into pMAL (pILL927, figure 2). Competent cells of E. coli MC1061 were transformed with the ligation reaction.

H. felis ureB was cloned in a two-step procedure, that allowed the production of both complete and truncated versions of the UreB subunit. Plasmid pILL213 (table 3) was digested with the enzymes DraI, corresponding to amino acid residue number 219 of the UreB subunit and HindIII. The resulting 1350 bp fragment was purified and cloned into pMAL that had been digested with XmnI and HindIII (pILL219, figure 2). In order to produce a clone capable of synthesizing a complete UreB protein, PCR primers were developed (set #3, table 2) that amplified a 685 bp fragment from the N-terminal portion of the ureB gene (excluding the ATG codon), that also overlapped the beginning of the insert in plasmid pILL219. The PCR amplified material was purified and digested with bamHI and HindIII, and then cloned into pMAL (pILL221, figure 14). A 1350 bp PstI-PstI fragment encoding the remaining portion of the UreB gene product was subsequently excised from pILL219 and cloned into a

linearised preparation of pILL221 (pILL222, figure 14).

Expression of recombinant urease polypeptides in the vector pMAL :

The expression vector pMAL is under the control of an inducible promoter (P_{lac}) and contains an open-reading frame (ORF) that encodes the production of MalE (Maltose-binding protein, MBP). Sequences cloned in-phase with the latter ORF resulted in the synthesis of MBP-fused proteins which were easily purified on amylose resin. Of the two versions of pMAL that are commercially available, the version not encoding a signal sequence (ie. pMAL-c2) synthesized greater amounts of recombinant proteins and was thus used throughout.

E. coli clones harbouring recombinant plasmids were screened for the production of fusion proteins, prior to performing large-scale purification experiments.

Purification of recombinant urease polypeptides :

Fresh 500 mL volumes of Luria broth, containing carbenicillin (100 μ g/mL and 2% (wt/vol) glucose, were inoculated with overnight cultures (5 mL) of E. coli clones. The cultures were incubated at 37° C and shaken at 250 rpm, until the $A_{600} = 0.5$. Prior to adding 1 mmol/L (final concentration) isopropyl- β -D-thiogalactopyranoside (IPTG) to cultures, a 1.0 mL sample was taken (non-induced cells). Cultures were incubated for a further 4 h at which time another 1.0 mL sample (induced cells) was taken. The non-induced and induced cell samples were later analysed by SDS-PAGE.

IPTG-induced cultures were centrifuged at 7000 rpm for 20 min, at 4° C and the supernatant discarded. Pellets were resuspended in 50 mL column buffer (200 mmol/L NaCl, 1 mmol/L EDTA in 10 mmol/L TrisHCl, pH 7.4), containing the following protease inhibitors (supplied by Boehringer, Mannheim, Germany) : 2 μ mol/L leupeptin, 2 μ mol/L pepstatin and 1 mmol/L phenylmethylsulphonyl fluoride (PMSF). Intact cells were lysed by passage through a French Pressure cell (16 000 lb/in²). Cell debris was removed by centrifugation and lysates were diluted in column buffer to give a final concentration of 2.5 mg protein/mL, prior to chromatography on a 2.6 cm x 20 cm column of amylose resin (New England Biolabs). The resin was washed with column buffer at 0.5 mL/min until the A₂₈₀ returned levels. The MBP-fused recombinant proteins were eluted from the column by washing with column buffer containing 10 mmol/L l-maltose.

Fractions containing the recombinant proteins were pooled and then dialysed several times at 4° C against a low salt buffer (containing 25 mmol/L NaCl in 20 mmol/L TrisHCl, pH 8.0). The pooled fractions were then loaded at a flow rate of 0.5 mL/min onto a 1.6 x 10 cm anion exchange column (HP-Sepharose , Pharmacia, Sweden) connected to a Hi-Load chromatography system (Pharmacia). Proteins were eluted from the column using a salt gradient (25 mmol/L to 500 mmol/L NaCl). Fractions giving high absorbance readings at A₂₈₀ were exhaustively dialysed against distilled water at 4° C and analysed by SDS-PAGE.

Rabbit antisera :

Polyclonal rabbit antisera was prepared against total cell extracts of H. pylori strain 85P (Labigne et al., 1991) and H. felis (ATCC49179). Polyclonal rabbit antisera against recombinant protein preparations of H. pylori and H. felis urease subunits was produced by immunizing rabbits with 100 µg of purified recombinant protein in Freund's complete adjuvant (Sigma). Four weeks later, rabbits were booster-immunized with 100 µg protein in Freund's incomplete adjuvant. On week 6, the animals were terminally bled and the sera kept at -20° C.

Protein analyzes by SDS-PAGE and western blotting :

Solubilized cell extracts were analyzed on slab gels, comprising a 4.5% acrylamide stacking gel and a 10% resolving gel, according to the procedure of Laemmli. Electrophoresis was performed at 200 V on a mini-slab gel apparatus (Bio-Rad, USA).

Proteins were transferred to nitrocellulose paper in a Mini Trans-Blot transfer cell (Bio-Rad) set at 100 V for 1 h, with cooling. Nitrocellulose membranes were blocked with 5% (wt/vol) casein (BDH, England) in phosphate-buffered saline (PBS, pH 7.4) with gentle shaking at room temperature, for 2 h. Membranes were reacted at 4° C overnight with antisera diluted in 1% casein prepared in PBS. Immunoreactants were detected using specific biotinylated secondary antibodies and streptavidin-peroxidase conjugate (Kirkegaard and Parry Lab., Gaithersburg, USA). Reaction products were visualized on autoradiographic film (Hyperfilm, Amersham, France) using a chemiluminescence technique (ECL system, Amersham).

Protein concentrations were determined by the Bradford assay (Sigma Chemicals corp., St Louis, USA).

Animal experimentation :

Six week old female Swiss Specific Pathogen-Free (SPF) mice were obtained (Centre d'Elevage R. Janvier, Le-Genest-St-Isle, France) and maintained on a commercial pellet diet with water ad libitum. The intestines of the animals were screened for the absence of Helicobacter muridarum. For all orogastric administrations, 100 μ L aliquots were delivered to mice using 1.0 mL disposable syringes, to which polyethylene catheters (Biotrol, Paris, France) were attached.

Preparation of sonicated extracts and inocula from *H. felis* cultures :

H. felis bacteria were harvested in PBS and centrifuged at 5000 rpm, for 10 min in a Sorvall RC-5 centrifuge (Sorvall, USA) at 4° C. The pellets were washed twice and resuspended in PBS. Bacterial suspensions were sonicated as previously described and were subjected to at least one freeze-thaw cycle. Protein determinations were carried out on the sonicates.

To ensure a virulent culture of H. felis for protection studies, H. felis bacteria were maintained in vivo until required. Briefly, mice were inoculated three times (with 10^{10} bacteria/mL), over a period of 5 days. The bacteria were reisolated from stomach biopsies on blood agar medium (4 - 7 days' incubation in a microaerobic atmosphere at 37° C). Bacteria grown for two days on blood agar plates were harvested directly in peptone water (Difco, USA). Bacterial viability and motility was assessed by phase microscopy prior to administration to animals.

Mouse protection studies :

Fifty μg of recombinant antigen and 10 μg cholera holotoxin (Sigma Chemical Corp.), both resuspended in HCO_3 , were administered orogastrically to mice on weeks 0, 1, 2 and 3. Mice immunized with sonicated H. felis extracts (containing 400 - 800 μg of total protein) were also given 10 μg of cholera toxin. On week 5, half of the mice from each group were challenged with an inoculum of virulent H. felis. The remainder of the mice received an additional "boost" immunization on week 15. On week 17 the latter were challenged with a culture of H. felis.

Assessment of H. felis colonisation of the mouse :

Two weeks after receiving the challenge dose (ie. weeks 7 and 19, respectively) mice were sacrificed by spinal dislocation. The Stomachs were washed twice in sterile 0.8% NaCl and a portion of the gastric antrum from each stomach was placed on the surfaces of 12 cm x 12 cm agar plates containing a urea indicator medium (2% urea, 120 mg Na_2HPO_4 , 80 mg KH_2PO_4 , 1.2 mg phenol red, 1.5 g agar prepared in 100 mL). The remainder of each stomach was placed in formal-saline and stored until processed for histology. Longitudinal sections (4 μm) of the stomachs were cut and routinely stained by the Giemsa technique. When necessary, sections were additionally stained by the Haematoxylin-Eosin and Warthin-Starry silver stain techniques;

The presence of H. felis bacteria in mouse gastric mucosa was assessed by the detection of urease activity (for up to 24 h) on the indicator medium, as well as by the screening of Giemsa-stained gastric sections that had been coded so as to eliminate observer bias. The numbers of bacteria in gastric sections were semi-quantitatively scored according to the following scheme : 0, no bacteria seen throughout

sections ; 1, few bacteria (< 20) seen throughout ; 2, occasional high power (H.P.) field with low numbers (< 20) of bacteria ; 3, occasional H.P. field with low to moderate numbers (< 50) of bacteria ; and 4, numerous (> 5) H.P. fields with high numbers of bacteria (> 50). Mononuclear cell infiltrates were scored as follows : 0, no significant infiltration ; 1, infiltration of low numbers of mononuclear cells limited to the submucosa and muscularis mucosa ; 2, infiltration of moderate numbers of mononuclear cells to the submucosa and muscularis mucosa, sometimes forming loose aggregates ; and 3, infiltration of large numbers of mononuclear cells and featuring nodular agglomerations of cells.

RESULTS OF PART II EXPERIMENTS :

Expression of Helicobacter urease polypeptides in E. coli :

Fragments containing the sequences encoding the respective UreA gene products of H. felis and H. pylori were amplified by PCR and cloned in-phase with an ORF encoding the 42 kDa MBP, present on the expression vector pMAL. Sequencing of the PCR products revealed minor nucleotidic changes that did not, however, alter the deduced amino acid sequences of the respective gene products. E. coli MC1061 cells transformed with these recombinant plasmids (pILL919 and pILL920, respectively) expressed fusion proteins with predicted molecular weights of approximately 68 kDa. Following chromatography on affinity (amylose resin) and anion exchange gel media (Q-Sepharose), these proteins were purified to high degrees of purity (figure 1). The yield from 2-L cultures of recombinant

E. coli cells was approximately 40 mg of purified antigen.

Similarly, the large UreB subunits of H. pylori and H. felis ureases were expressed in E. coli (plasmids pILL927 and pILL222, respectively) and produced fusion proteins with predicted molecular weights of 103 kDa. The yield in these cases was appreciably lower than for the UreA preparations (approximately 20 mg was recovered from 2-L of bacterial culture). Moreover, problems associated with the cleavage of the UreB polypeptides from the MBP portion of the fusion proteins were encountered. These difficulties were attributed to the large sizes of the recombinant UreB polypeptides.

Analysis of the recombinant urease polypeptides :

Western blot analyses of the antigen preparations with rabbit polyclonal antisera raised to whole-extracts of H. pylori and H. felis bacteria demonstrated that the antigens retained immunogenicity to the homologous as well as heterologous antisera (figures 14 and 15). The antisera did not recognize the MBP component alone. Cross-reactivity between the urease polypeptides of H. pylori and H. felis was consistent with the high degrees of identity between the amino acid sequences of these proteins.

Rabbit polyclonal antisera raised against purified recombinant UreA and UreB proteins prepared from H. pylori and H. felis strongly reacted with the urease polypeptides present in whole-cell extracts of the bacteria (figure 16). As we had already observed, the UreB subunit of H. felis urease migrated slightly higher on SDS-PAGE gels than did that of H. pylori (figure 16).

Preparation of *H. felis* inocula used in immunoprotection studies :

To ensure the virulence of *H. felis* bacterial inocula, bacteria were reisolated from *H. felis*-infected mouse stomachs (see Materials and methods). The bacteria were passaged a minimum number of times in vitro. Stock cultures prepared from these bacteria, and stored at -80° C, were used to prepare fresh inocula for other mouse protection studies. This procedure ensured that the inocula used in successive experiments were reproducible.

Immunization of mice against gastric *H. felis* infection :

Mice that had been immunized for three weeks with the given antigen preparations were divided into two lots and one half of these were challenged two weeks later with an *H. felis* inoculum containing 10⁷ bacteria/mL. One group of animals that had been immunized with recombinant *H. felis* UreA were also challenged but, unlike the other animals, were not sacrificed until week 19.

a) Protection at week 5 :

Eighty-five % of stomach biopsy samples from the control group of mice immunized with *H. felis* sonicate preparations were urease-negative and therefore appeared to have been protected from *H. felis* infection (table 4). This compared to 20% of those from the other control group of animals given MBP alone. The proportion of urease-negative stomachs for those groups of mice given the recombinant urease subunits varied from 70% (for *H. pylori* UreB) to 20% (for *H. pylori* UreA).

The levels of bacterial colonisation by H. felis was also assessed from coded histological slides prepared from gastric tissue. Due to the striking helical morphology of H. felis bacteria, the organisms could be readily seen on the mucosal surfaces of both gastric pit and glandular regions of the stomach. Histological evidence indicated that the levels of protection in mice was lower than that observed by the biopsy urease test : 25% and 20% of gastric tissue from mice immunized with H. felis sonicate preparations of H. pylori UreB, respectively, were free of H. felis bacteria.

Amongst certain groups of these mice the preponderance of urease-negative biopsies, as well as lower histological scores for bacterial colonisation (unpublished data), suggested that an immunoprotective response had been elicited in the animals. This response, however, may have been insufficient to protect against the inoculum administered during the challenge procedure.

b) Protection at week 17 :

The remaining mice, from each group of animals, were boosted on week 15. These mice were challenged at week 17 with an H. felis inoculum containing approximately 100-fold less bacteria than that used previously. Two weeks later all stomach biopsies from the MBP-immunized mice were urease-positive (table 4). In contrast, urease activity for gastric biopsies from mice immunized with the recombinant urease subunits varied from 50% for H. pylori UreA to 100% for H. felis UreB. The latter was comparable to the level of protection observed for the group of animals immunized with H. felis sonicated extracts. Histological evidence demonstrated that the UreB subunits of H.

felis and H. pylori protected 60% and 25% of immunized animals, respectively. This compared with a level of 85% protection for mice immunized with H. felis sonicated extracts. Immunization of mice with recombinant H. pylori UreA did not protect the animals. Similarly, the stomachs of all H. felis UreA-immunized mice, that had been challenged at week 5, were heavily colonised with H. felis bacteria at week 19 (table 4).

The urease gastric biopsy test, when compared to histological analysis of gastric tissue sections, gave sensitivity and specificity values of 63% and 95%, respectively. Thus histology proved to be the more accurate predictor of H. felis infection in the mouse.

Cellular immune response in immunized stomachs :

In addition to the histological assessment of H. felis colonisation, mouse gastric tissue was also scored (from 0 to 3) for the presence of a mononuclear cell response. In mice immunized with MBP alone, a mild chronic gastritis was seen with small numbers of mononuclear cells restricted to the muscularis mucosa and to the submucosa of the gastric epithelium. In contrast, there were considerable numbers of mononuclear cells present in the gastric mucosae from animals immunized with either the recombinant urease polypeptides, or with H. felis sonicate preparations. These inflammatory cells coalesced to form either loose aggregates, in the submucosal regions of the tissue, or nodular structures that extended into the mucosal regions of the gastric epithelia. The mononuclear cell response did not appear to be related to the presence of bacteria as the gastric mucosae from the H. felis UreA-immunized mice, that were

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heavily colonized with H. felis bacteria, contained little or no mononuclear cells.

Table 2 The oligomeric primers used in PCR-based amplification of urease-encoding nucleotide sequences.

Primer set		Nucleotide sequence (5' -> 3')
# 1	forw	...CAU CCT [*] AAA ^G GAA ^G T ^C TA [*] GAT ^C AAA ^G T ^C TA [*] ATG
	rev	T ^C TC C ^T TT A [*] CG A [*] CG A [*] G ^C AT A ^{G,T} AT C ^T TT C ^T TT CAT CUA...
#2	forw	CC GGA <u>GAA TTC</u> ATT AGC AGA AAA GAA TAT GTT TCT ATG <i>EcoRI</i> [¥]
	rev	AC GTT <u>CTG CAG</u> CTT ACG AAT AAC TTT TGT TGC TTG ACC <i>PstI</i> [¥]
#3	forw	<u>GGA TCC</u> AAA AAG ATT TCA CG <i>BamHI</i> [¥]
	rev	GGA AGC <u>TT C TGC</u> AGG TGT GCT TCC CCA GTC <i>HindIII</i> [¥] <i>PstI</i> [¥]

* Degenerated nucleotides in which all possible permutations of the genetic code were included (A, T, G, C).

G,C,T The given nucleotides were degenerated with the specific base(s) shown.

¥ Restriction sites introduced in the amplified fragments.

Table 3 Plasmids used

Plasmid	Vector	Relevant phenotype or character	Reference
pILL763	pILL570	9.5 kb fragment (<i>Sau</i> 3a partial digest of <i>H. pylori</i> chromosome) (Sp ^R)	Cussac <i>et al.</i> , 1991
pILL199	pILL575	35 kb fragment (<i>Sau</i> 3A partial digest of <i>H. felis</i> chromosome)	Ferrero & Labigne, '93
pILL207	pILL570	11 kb fragment (<i>Sau</i> 3A partial digest of pILL199)	This study
pILL919	pMAL-C2	0.8 kb <i>Bam</i> HI- <i>Pst</i> I ^a insert containing a nucleotide fragment encoding <i>H. felis ureA</i> gene (Ap ^R)	This study
pILL920	pMAL-C2	0.8 kb <i>Bam</i> HI- <i>Pst</i> I ^a insert containing PCR product encoding <i>H. pylori ureA</i> gene	This study
pILL927	pMAL-C2	1.8 kb <i>Eco</i> RI- <i>Pst</i> I ^a PCR fragment encoding <i>H. pylori ureB</i> gene	This study
pILL213	pUC19	2 kb fragment resulting from <i>Sau</i> 3A partial digest of pILL207 (Ap ^R)	This study
pILL219	pMAL-C2	1.4 kb <i>Dra</i> I- <i>Hind</i> III ^b insert containing <i>H. felis ureB</i> (bases 657 - 1707)	This study
pILL 221	pMAL-C2	0.7 kb <i>Bam</i> HI- <i>Pst</i> I PCR fragment encoding <i>H. felis ureB</i> (bases 4 - 667)	This study
pILL222	pMAL-C2	1.35 kb <i>Pst</i> I- <i>Pst</i> I ^c fragment encoding <i>H. felis ureB</i> (bases 667 - 1707) from pILL219 cloned into linerized pILL221	This study

Table 4 Protection of mice by immunization
with recombinant urease proteins.

Antigen	Protection (%) ^a	
	Urease	Histology
MBP	0 % (0/10)	0 % (0/10)
UreA <i>H. pylori</i>	50 (4/8)	0 (0/10)
UreA <i>H. felis</i> ^b	12.5 (1/8)	0 (0/10)
UreB <i>H. pylori</i>	65 (5/8)	25 (2/8)
UreB <i>H. felis</i>	100 (7/7)	60 (5/7)
<i>H. felis</i> sonicate	100 (8/8)	85 (7/8)

^a Challenge inoculum dose was 10^5
bacteria/mouse

^b Mice were challenged on week 5 (with 10^7
bacteria) and were sacrificed on week 19.

III- HELICOBACTER PYLORI hspA-B HEAT SHOCK GENE
CLUSTER : NUCLEOTIDE SEQUENCE, EXPRESSION AND
FUNCTION :

A homolog of the heat shock proteins (HSPs) of the GroEL class, reported to be closely associated with the urease of *Helicobacter pylori* (a nickel metalloenzyme), has recently been purified from *H. pylori* cells by Dunn et al, and Evans et al. (Infect. Immun. 60:1946, 1992, 1946 and 2125, respectively). Based on the reported N-terminal amino acid sequence of this immunodominant protein, degenerated oligonucleotides were synthesized in order to target the gene (hspB) encoding the GroEL-like protein in the chromosome of *H. pylori* strain 85P. Following gene amplification, a 108-base pair (bp)-fragment encoding the 36 first amino acids of the HspB protein was purified, and used a probe to identify in the *H. pylori* genomic bank a recombinant cosmid harboring the entire HspB encoding gene. The hspB gene was mapped to a 3.15 kilobases (kb) BglIII restriction fragment of the pILL684 cosmid. The nucleotide sequence of that fragment subcloned into the pILL570 plasmid vector (pILL689) revealed the presence of two open reading frames (ORFs) designated hspA and hspB, the organization of which was very similar to be groESL bicistronic operons of other bacterial species. hspA and hspB encode polypeptides of 118 and 545 amino acids respectively, corresponding to calculated molecular masses of 13.0 and 58.2 kilodaltons (kDa), respectively. Amino acid sequence comparison studies revealed i) that the *H. pylori* HspA and HspB protein were highly similar to their bacterial homologs; ii) that the HspA *H. pylori* protein features a striking motif at the carboxyl terminus that other bacterial

GroEs-homologs lack ; this unique motif consists of a series of eight histidine residues resembling metal binding domain, such a nickel binding. Surprisingly, immediately upstream of the gene cluster an IS5 insertion element was found that was absent in the *H. pylori* genome, and was positively selectionned during the cosmid cloning process. The IS5 was found to be involved in the expression of the hspA and hspB genes in pILL689. The expression of the HspA and HspB proteins from the pILL689 plasmid was analyzed in minicell-producing strain. Both polypeptides were shown to be constitutively expressed in the *E. coli* cells. When the pILL689 recombinant plasmid was introduced together with the *H. pylori* urease gene cluster into an *E. coli* host strain, an increase of urease activity was observed suggesting a close interaction between the heat shock proteins and the urease enzyme. Supporting the concept of a specific function for the HspA chaperone, was the fact that whereas a single hspB copy was found in the *H. pylori* genome, two copies of the hspA were found in the genome, one linked to the hspB gene and one unlinked to the hspB gene. Attempts to construct isogenic mutants of *H. pylori* in the hspA and the hspB gene were unsuccessful suggesting that these genes are essential for the survival of the bacteria.

EXPERIMENTAL PROCEDURES FOR PART III :

Bacterial strains, plasmids, and culture conditions :

The cloning experiments were performed with genomic DNA prepared from *H. pylori* strain 85P. *H. pylori* strain N6 was used as the recipient strain for the electroporation experiments because of its favorable transformability. *E. coli* strain HB101 or

strain MC1061 were used as a host for cosmid cloning and subcloning experiments, respectively. *E. coli* P678-54 was used for preparation of minicells. Vectors and recombinant plasmids used in this study are listed in Table 1. *H. pylori* strains were grown on horse blood agar plates, supplemented with vancomycin (10 mg/l), polymyxin B (2,500 U/I), trimethoprim (5 mg/l), and amphotericin B (4 mg/l). Plates were incubated at 37°C under microaerobic conditions in an anaerobic jar with a carbon dioxide generator envelope (BBL 70304). *E. coli* strains were grown in L-broth without glucose (10 g of tryptone, 5 g of yeast extract, and 5 g of NaCl per liter ; pH 7.0) or on L-agar plates (1.5 % agar) at 37°C. For measurement of urease activity, the nitrogen-limiting medium used consisted of ammonium-free M9 minimal agar medium (pH7.4) containing 0.4 % D-glucose as the carbon source, and freshly prepared filter-sterilized L-arginine added to the final concentration of 10 mM. Antibiotic concentrations for the selection of recombinant clones were as follows (in milligrams per liter) : kanamycin, 20 ; spectinomycin, 100 ; carbenicillin, 100.

Preparation of DNA :

Genomic DNA from *H. pylori* was prepared as previously described. Cosmid and plasmid DNAs were prepared by an alkaline lysis procedure followed by purification in cesium chloride-ethidium bromide gradients as previously described.

Cosmid cloning :

The construction of the cosmid gene bank of *H. pylori* 85P in *E. coli* HB101, which was used for the cloning of the *H. pylori* hspA-B gene cluster, has been described previously.

DNA analysis and cloning methodology :

Restriction endonucleases, T4 DNA ligase, DNA polymerase I large (Klenow) fragment, and Taq polymerase were purchased from Amersham, T4 DNA polymerase from Biolabs, and calf intestinal phosphatase from Pharmacia. All enzymes were used according to the instructions of the manufacturers. DNA fragments were separated on agarose gels run in Tris-acetate buffer. The 1-kb ladder from Bethesda Research Laboratories was used as a fragment size standard. When necessary, DNA fragments were isolated by electroelution from agarose gels as previously described and recovered from the migration buffer by means of an Elutip-d minicolumn (Schleicher and Schuell, Dassel, Germany). Basic DNA manipulations were performed according to the protocols described by Sambrook et al.

Hybridization :

Colony blots for screening of the *H. pylori* cosmid bank and for identification of subclones were prepared on nitrocellulose membranes (Schleicher and Schuell, Dassel, Germany) according to the protocol of Sambrook et al. (43). Radioactive labelling of PCR-products was performed by random priming, using as primers the random hexamers from Pharmacia. Colony hybridizations were performed under high stringency conditions (5 x SSC, 0.1 % SDS, 50 % formamide, 42° C) (1 x SSC ; 150 mM NaCl, 15 mM sodium citrate, pH 7.0). For Southern blot hybridizations, DNA fragments were transferred from agarose gels to nitrocellulose sheets (0.45- μ m pore size ; Schleicher & Schuell, Inc.), and hybridized under low stringency conditions (5 x SSC, 0.1 % SDS, 30 or 40 % formamide, at 42° C with ³²P-labeled deoxyribonucleotide probes Hybridization was

revealed by autoradiography using Amersham Hyperfilm-MP.

DNA sequencing :

Appropriate fragments of plasmid DNA were subcloned into M13 mp 18/19 vectors. Single stranded DNA was prepared by phage infection of E. coli strain JM101. Sequencing was performed by the dideoxynucleotide chain termination method using the United States Biochemicals Sequenase kit. Both the M13 universal primer and additional specific primers (Fig.1) were used to sequence both the coding and non-coding DNA strands. Sequencing of double-stranded DNA was performed as previously described. Direct sequencing of PCR product was carried out following purification of the amplified, electroeluted PCR product through an Elutip-d minicolumn (Schleicher & Schuell) ; The classical protocol for sequencing using the Sequenase kit was then used with the following modifications : PCR product was denatured by boiling annealing mixture containing 200 picomoles of the oligonucleotide used as primer and DMSO to the final concentration of 1 % for 3 minutes ; the mixture was then immediately cool on ice ; the labeling step was performed in presence of manganese ions (mM).

Electroporation of H. pylori :

In the attempt to construct H. pylori mutants, appropriate plasmid constructions carrying the targeted gene disrupted by a cassette containing a kanamycin resistance gene (aph3'-III), were transformed into H. pylori strain N6 by means of electroporation as previously described. Plasmid pSUS10 harboring the kanamycin disrupted flaA gene was used as positive control of electroporation. After

electroporation, bacteria were grown on non-selective plates for a period of 48 h in order to allow for the expression of the antibiotic resistance and then transferred onto kanamycin-containing plates. The selective plates were incubated for up to 6 days.

Polymerase chain reaction (PCR) :

PCRs were carried out using a Perkin-Elmer Cetus thermal cycler using the GeneAmp kit (Perkin-Elmer Cetus). Classical amplification reaction involved 50 picomoles (pmoles) of each primer and at least 5 pmoles of the target DNA. The target DNA was heat denatured prior addition to the amplification reaction. Reaction consisted of 25 cycles of the following three steps : denaturation (94° C for 1 minute), annealing (at temperatures ranging between 42 and 55° C, depending on the calculated melting temperatures of the primers, for 2 min), and extension (72° C for 2 min). When degenerated oligonucleotides were used in non stringent conditions, up to 1000 pmoles of each oligonucleotide were added, 50 cycles were carried out, and annealing was performed at 42° C.

Analysis of proteins expressed in minicells :

Minicells harboring the appropriate hybrid plasmid were isolated and labeled with [³⁵S] methionine (50 µ Ci/ml). Approximately 100,000 cpm of acetone-precipitable material was subjected to sodium dodecyl sulfate (SDS) -polyacrylamide gel electrophoresis in a 12.5 % gel. Standard proteins with molecular weights ranging from 94,000 to 14,000 (low molecular-weights kit from Bio-Rad Laboratories) were run in parallel. The gel was stained and examined by fluorography, using En³Hance (New England Nuclear).

Urease activity :

Urease activity was quantitated by the Berthelot reaction by using a modification of the procedure which has already been described. Urease activity was expressed as micromoles of urea hydrolyzed per minute per milligram of bacterial protein.

RESULTS OF PART III EXPERIMENTS :**Identification of a recombinant cosmid harboring the Helicobacter pylori GroEL-like heat shock protein encoding gene :**

Based on the published N-terminal amino sequence of the purified heat shock protein of *H. pylori*, two degenerated oligonucleotides were synthesized to target the gene of interest in the chromosome of *H. pylori* strain 85P. The first one 5' - G C N A A R G A R A T H A A R T T Y T C N G - 3' where N stands for the four nucleotides, R = A and G, Y = T and C, H = T, C, and A, is derived from for the first 8 amino acids of the protein (AKEIKFSD) ; the second one 5' - C R T T N C K N C C N C K N G G N C C C A T - 3', where K = G and T, corresponds to the complementary codons specifying the amino acid from position 29 to position 36 (MGPRGRNV, ref). The expected size for the PCR product was 108 base pairs (bp). The amplification reaction was performed under low stringency conditions as described in the "Materials and Methods" section, and led to the synthesis of six fragments with size ranging from 400 bp to 100 bp. The three smallest fragments were electroeluted from an acrylamide gel, and purified. Direct sequencing of the PCR products permitted the identification of a DNA fragment encoding an amino acid sequence corresponding to the published sequence. This fragment was therefore

labeled and used as probe in colony hybridization to identify recombinant cosmids exhibiting homology to a 5' segment of the *H. pylori* GroEL-like encoding gene ; this gene was further designated hspB. The gene bank consists of 400 independent kanamycin-resistant *E. coli* transductants harboring recombinant cosmids. Of those one single clone hybridized with the probe, and harbored a recombinant plasmid designated pILL684, 46 kb in size. The low frequency observed when detecting the hspB gene (1 of 400) was unusual when compared with that of several cloned genes which were consistently detected in five to seven recombinant cosmids. In order to identify the hspB gene, fragments with sizes of 3 to 4 kb were generated by partial restriction of the pILL684 cosmid DNA with endonuclease Sau3A, purified, and ligated into the BglII site of plasmid vector pILL570. Of 100 subclones, x were positive clones, and one was further studied (pILL689) ; it contains a 3.15 kb insert, flanked by two BglII restriction sites, that was mapped in detail (Fig. 5). Using the PCR ³²P labeled probe, the 5' end of the hspB gene was found to map to the 632 bp HindIII-SphI central restriction fragment of pILL689, indicating that one could expect the presence of the entire hspB gene in the pILL689 recombinant plasmid.

DNA sequence and deduced amino acid sequence of the *H. pylori* hspA-B gene cluster :

The 3200 bp of pILL689 depicted in Fig. 5 were sequenced by cloning into M13mp18 and M13mp19, the asymmetric restriction fragments BglII-SphI, SphI-HindIII, HindIII-BglII ; each cloned fragment was independently sequenced on both strands 16 oligonucleotide primers (Fig.1) were synthesized to

confirm the reading and/or to generate sequences overlapping the independently sequenced fragments ; these were used as primers in double-stranded-DNA sequencing analyses.

The analysis of the sequence revealed two distinct genetic elements. First the presence of two open reading frames (ORFs), depicted in figure 5, transcribed in the same direction, that were designated hspA and hspB ; The nucleotide sequence and the deduced amino acid sequence of the two ORFs are presented in Fig. 6. The first codon of hspA begins 323 bp upstream of the leftward HindIII site of pILL689 (Fig. 5) and is preceded by a Shine-Dalgarno ribosome-binding site (RBS) (GGAGAA). The hspA ORF codes for a polypeptide of 118 amino acids. The initiation codon for the hspB ORF begins 25 nucleotides downstream the hspA stop codon ; it is preceded by a RBS site (AAGGA). The hspB ORF encodes a polypeptide of 545 amino acids and is terminated by a TAA codon followed by a palindromic sequence resembling a rho-independent transcription terminator (free energy, $\Delta G = -19.8$ kcal/mol) (Fig. 6). The N-terminal amino acid sequence of the deduced protein HspB was identical to the N-terminal sequence of the purified *H.pylori* heat shock protein previously published with the exception of the N-terminal methionine, which is absent from the purified protein and might be posttranslationally removed, resulting in a mature protein of 544 amino acids.

The deduced amino acid sequences of *H. pylori* HspA and HspB were compared to several amino acid sequences of HSPs of the GroES and GroEL class (Fig. 7). HspB exhibited high homology at the amino acid level with the *Legionella pneumophila* HtpB protein (82.9 % of similarities), with the *Escherichia coli*

GroEL protein (81.0 % of similarities), with the *Chlamydia psittaci* or *C. trachomatis* HspB protein (79.4 % of similarities), with *Clostridium perfringens* Hsp60 protein (80.7 % of similarities), and to a lesser extent to the GroEL-like proteins of *Mycobacterium*. However, like almost all the GroEL homologs, *H. pylori* HspB demonstrated the conserved carboxyl-terminus glycine-methionine motif (MGGMGGMGGMGGM) which was recently shown to be dispensable in the *E. coli* GroEL chaperonin. The degree of homology at the amino acid level between the *H. pylori* HspA protein and the other GroES-like proteins is shown in Fig. 7. The alignment shown features a striking motif at the carboxyl terminus of the *H. pylori* HspA protein that other bacterial GroES-homologs lack. This unique highly charged motif consists of 27 additional amino acids capable of forming a loop between two double cysteine residues; of the 27 amino acids, 8 are histidine residues highly reminiscent of a metal binding domain.

The second genetic element revealed by the sequence analysis, was the presence of an insertion sequence (IS5) 84 bp upstream of the hspA gene. The nucleotide sequence of this element matched perfectly that previously described for IS5 in *E. coli*, with the presence of a 16 nucleotide sequence (CTTGTTGCGCACCTTCC) that corresponds to one of the two inverted repeats which flank the IS5 element. Because of the perfect match at the DNA level, we suspected that the IS5 was not initially present in the *H. pylori* chromosome, but had rather inserted upstream of the hspA-HspB gene cluster during the cloning process, a hypothesis that needed to be confirmed by further analyses.

Identification of the upstream sequence of the hspA-B gene cluster in H. pylori chromosome :

The presence of the IS5 was examined by gene amplification using two oligonucleotides, one being internal to the IS5 element and the other one downstream of the IS5 element (oligo #1 and #2, Fig. 6), to target a putative sequence i) in the chromosome of H. pylori strain 85P, ii) in the initial cosmid pILL684, and iii) in the 100 subclones resulting of the Sau3A partial restriction of the pILL684 recombinant cosmid. IS5 was absent from the chromosome of H. pylori, and was present in the very first subcultures of the E. coli strain harboring cosmid pILL684. Among the 100 pILL684 subclone derivatives which appeared to contain all or part of the IS5 sequence, we then looked for a subclone harboring the left end side of the IS5 plus the original upstream sequence of the hspA-hspB gene cluster. This screening was made by restriction analysis of the different Sau3A partial generated subclones. The restriction map of one (pILL694) of the plasmids fulfilling these criteria is shown in Fig. 5. The left end side of the IS5 nucleotide sequence was determined ; the presence of a 4-bp duplication CTAA on both side of the 16-bp inverted repeats of the IS5 element (Fig. 6) allowed us to confirm the recent acquisition of the IS5 element by transposition. A 245-nucleotide sequence was then determined that mapped immediately upstream of the IS5 element (shown Fig. 6). This sequence consists of a non coding region in which the presence of a putative consensus heat shock promoter sequence was detected ; it shows a perfectly conserved -35 region (TAACTCGCTTGAA) and a less consentaneous -10 region (CTCAATTA). Two oligonucleotides (#3 and #4, shown on Fig.2) were synthesized which mapped to

sequences located on both side of the IS5 element present in the recombinant cosmid ; these two oligonucleotides should lead to the amplification of a XXXXbp fragment when the IS5 sequence is present and a fragment in the absence of the IS5. The results of the PCR reaction using as target DNA the pILL684 cosmid, the pILL694 plasmid, and the *H. pylori* 85P chromosome fit the predictions (results not shown). Moreover, direct sequencing of the PCR product obtained from the *H. pylori* chromosome was performed and confirmed the upstream hspA-hspB reconstructed sequence shown in Fig. 6 (B). To further confirm the genetic organization of the whole sequenced region, two probes were prepared by gene amplification of the pILL689 plasmid using oligonucleotides #5 and #6, and #7 and #8 (Fig. 6). ; they were used as probes in Southern hybridization experiments under low stringency conditions against an HindIII digest of the *H. pylori* 85P chromosome. The results demonstrate that no other detectable rearrangement had occurred during the cloning process (data not shown). These experiments allowed us to demonstrate that whereas a single copy of the hspB gene was present in the chromosome of *H. pylori* strain 85, two copies of the hspA gene were detected by Southern hybridization.

Analysis of polypeptides expressed in minicells :

The pILL689 and the pILL692 recombinant plasmids and the respective cloning vectors pILL570, and pACYC177, were introduced by transformation into *E. coli* P678-54, a minicell-producing strain. The pILL689 and pILL692 plasmids (Fig. 5) contain the same 3.15-kb insert cloned into the two vectors. pILL570 contains upstream of the poly-cloning site a stop of transcription and of translation ; the orientation of

the insert in pILL689, was made in such way that the transcriptinnal stop was located upstream of the IS5 fragment and therefore upstream of the hspA and HspB genes. Two polypeptides that migrated with polypeptides having apparent molecular weights of 60 kDa and 14 kDa were clearly detected in minicell-experiments from pILL689 and pILL692 (results not shown), whereas they were absent from the corresponding vectors ; these results indicated that the hspA and hspB genes were constitutively expressed from a promoter located within the IS5 were constitutively expressed from a promoter located within the IS5 element. Moreover, whereas the amount of polypeptides visualized on the SDS gel was in good agreement with the copy number of the respective vectors, the intensity of the two polypeptidic bands suggested a polycistronic transcription of the two genes.

Attempts to understand the role of the Hspa and HspB proteins :

Two disruptions of genes were achieved in E. coli by inserting the Km cassette previously described within the hspA or the hspB gene of plasmids pILL686 and pILL691. This was done in order to return the disrupted genes in *H. pylori* by electroporation, and to select for allelic replacement. The pILL696 resulting plasmid encoded a truncated form of the Hspa protein, corresponding to the deletion of the C-terminal end amino acid sequence ; in that plasmid the Km cassette was inserted in such way that the promoter of the Km gene could serve as promoter for the hspB downstream gene. The pILL687 and pILL688 plasmids resulted from the insertion of the Km cassette in either orientation within the hspB gene. None of these

constructs led to the isolation of kanamycin transformants of *H. pylori* strain N6, when purified pILL687, pILL688, pILL696 plasmids (Table 2, Fig. 5) were used in electroporation experiments, whereas the pSUS10 plasmid used as positive control always did. These results suggest the *H. pylori* HspA and HspB protein are essential proteins for the survival of *H. pylori*.

Because of i) the constant description in the literature of a close association of the HspB protein with the urease subunits ; -ii) the unique structure of the HspA protein with the C-terminal sequence reminiscent of a nickel binding domain, and iii) of the absence of viable hspA and/or hspB mutants of *H. pylori*, we attempted to demonstrate a role of the *H. pylori* Hsps proteins in relations with the *H. pylori* urease by functional complementation experiments in *E. coli*. Plasmids pILL763 or pILL753 (both pILL570 derivatives, Table 5) encoding the urease gene cluster were introduced with the compatible pILL692 plasmid (pACYC177 derivative) that constitutively expresses the HspA et HspB polypeptides as visualized in minicells. In both complementations, the expression of the HspA and HspB proteins in the same *E. coli* cell allows to observe a three fold increase in the urease activity following induction of the urease genes on minimum medium supplemented with 10 mM L- Arginine as limiting nitrogen source.

Table 5 : Vectors and hybrid plasmids used in this study.

Plasmid	Vector	Size (kb)	Characteristics (a)	Origin or Reference
pLL1575		10	Mob, Cos, Km	-
pLL1570		5.3	Mob, Sp	-
pACYC177		3.9	Ap, Km	-
pBR322		5.7	Ap, Km, source of Km-cassette	-
pLL1600		46	Mob, Km, cosmid containing <i>H. pylori</i> hspA-B	Sau3A partial digest of <i>H. pylori</i> 85P DNA
pLL1684		9.29	Mob, Sp, plasmid containing <i>H. pylori</i> hspB	Sau3A partial digest of pLL1684
pLL1685		4.5	Ap, plasmid containing <i>H. pylori</i> hspB	1.9-kb BglII-Clal pLL1685 cloned into pUC19*
pLL1686		5.9	Ap, Km, <i>H. pylori</i> hspB Ω Km-orientation A (b)	1.4-kb SmaI-SmaI pLL1600 cloned into pLL1686
pUC19*(c)		5.9	Ap, Km, <i>H. pylori</i> hspB Ω Km-orientation B (b)	1.4-kb SmaI-SmaI pLL1600 cloned into pLL1686
pLL1688		8.45	Mob, Sp, plasmid containing <i>H. pylori</i> hspA-B	Sau3A partial digest of pLL1684
pLL1689		3.9	Ap, plasmid containing <i>H. pylori</i> hspA 1.3-kb	SphI-SphI pLL1689 cloned into pUC19**
pLL1691		7.05	Ap, Km, plasmid containing <i>H. pylori</i> hspA-B	3.15-kb BglII pLL1689 cloned into pACYC177
pLL1692		8.7	Sp, plasmid containing left end of IS5	Sau3A partial digest of pLL1684
pLL1694		5.3	Ap, Km, <i>H. pylori</i> hspA Ω Km-orientation A (b)	1.4-kb SmaI-SmaI pLL1600 cloned into pLL1691
pLL1696		7.7	Ap, Km, <i>H. pylori</i> flaA Ω Km	-
pSUS10		16.5	Sp, plasmid containing <i>ureA</i> , B, C, D, E, F, G, H, I	-
pLL1753		14.75	Sp, plasmid containing <i>ureA</i> , B, E, F, G, H, I	-
pLL1763				

(a) Mob, conjugative plasmid due to the presence of OriT; Ap, Km, and Sp, resistance to ampicillin, kanamycin, and spectinomycin, respectively; Cos, presence of lambda cos site.

(b) Orientation A indicates that the Kanamycin promoter initiates transcription in the same orientation as that of the gene where the cassette has been inserted; orientation B, the opposite.

(c) pUC19* and pUC19** : derivatives from pUC19 vector in which the the *SphI* and *HindIII* site, respectively, have been end-filled by using the Klenow polymerase and self religated.

IV - EXPRESSION, PURIFICATION AND IMMUNOGENIC
PROPERTIES OF H. PYLORI HSPA AND HSPB :

EXPERIMENTAL PROCEDURE FOR PART IV :

Expression and purification of recombinant fusion proteins :

The MalE-HspA, and MalE-HspB fusion proteins were expressed following the cloning of the two genes within the pMAL-c2 vector as described in the "Results" section using the following primers :

oligo #1 ccggagaattcAAGTTTCAACCATTTAGGAGAAAGGGTC
oligo #2 acgttctgcagTTTAGTGTTTTTTGTGATCATGACAGC
oligo #3 ccggagaattcGCAAAGAAATCAAATTTTCAGATAGC
oligo #4 acgttctgcagATGATACCAAAAAGCAAGGGGGCTTAC

Two liters of Luria medium containing glucose (30%) and ampicillin (100 µg/ml) were inoculated with 20 ml of an overnight culture of strain MC1061 containing the fusion plasmid and incubated with shaking at 37°C. When the OD600 of the culture reached 0.5, IPTG (at a final concentration of 10 mM) was added, and the cells were incubated for a further 4 hours. Cells were harvested by centrifugation (5000 rpm for 30 min at 4°C), resuspended in 100 ml of column buffer consisting of 10 mM Tris-HCl, 200 mM NaCl, 1 mM EDTA supplemented with protease inhibitors [(Leupeptin (2µM) - Pepstatin (2µM) - PMSF (1mM) - Aprotinin (1:1000 dilution)], and passed through a French press. After centrifugation (10,000 rpm for 20 min at 4°C), the supernatant were recovered and diluted (2-fold) with column buffer. The lysate was filtered through a 0.2 µm nitrocellulose filter prior to loading onto a preequilibrated amylose resin (22 x 2.5 cm). The fusion proteins were eluted with a 10mM maltose solution prepared in column buffer, and the fractions

containing the fusion proteins were pooled, dialyzed against distilled water, and lyophilized. Fusion proteins were resuspended in distilled water at a final concentration of 2 mg of lyophilized material/ml, and stored at -20°C. Concentration and purity of the preparations were controlled by the Bradford protein assay (Sigma Chemicals) and SDS-PAGE analyses.

Nickel binding properties of recombinant proteins :

E. coli MC1061 cells, containing either the pMAL-c2 vector or derivative recombinant plasmids, were grown in 100 ml-Luria broth in the presence of carbenicillin (100 µg/ml). The expression of the genes was induced with IPTG for four hours. The cells were centrifuged and the pellet was resuspended in 2 ml of Buffer A (6M guanidine hydrochloride, 0.1 M NaH₂PO₄, 0.01MTris, pH8.0). After gentle stirring for one hour at room temperature, the suspensions were centrifuged at 10,000 g for 15 min at 4°C. A 1.6 ml aliquot of Nickel-Nitrilo-Tri-Acetic resin (Nickel-NTA, QIA express), previously equilibrated in Buffer A, was added to the supernatant and this mixture was stirred at room temperature for one hour prior to loading onto a column. The column was washed with 20 ml buffer A, then 30 ml buffer B (8M urea, 0.1M Na-phosphate, 0.01MTris-HCl, pH8.0). The proteins were eluted successively with the same buffer as buffer B adjusted to pH 6.3 (Buffer C), pH 5.9 (Buffer D) and pH 4.5 (Buffer E) and Buffer F (6M guanidine hydrochloride, 0.2M acetic acid). Fifty µl of each fraction were mixed with 50 µl of SDS buffer and loaded on SDS gels.

Human sera :

Serum samples were obtained from 40 individuals, 28 were H. pylori-infected patients as confirmed by a positive culture for H. pylori and histological examination of the biopsy, and 12 were uninfected patients. The sera were kindly provided by R. J. Adamek (University of Bochum, Germany).

Immunoblotting :

Upon completion of SDS-PAGE runs in a Mini-PROTEAN II electrophoresis cell, proteins were transferred to nitrocellulose paper in a Mini Trans-Blot transfer cell (Bio-Rad) set at 100 V for 1 h (with cooling). Immunostaining was performed as previously described (Ferrero et al., 1992), except that the ECL Western blotting detection system (Amersham) was used to visualize reaction products. Human sera and the rabbit antiserum, raised against a whole-cell extract of H. pylori strain 85P, were diluted 1:1000 and 1:5000, respectively, in 1% (w/v) casein prepared in phosphate-buffered saline (PBS, pH7.4).

Serological methods [enzyme-linked immunosorbent assay, (ELISA)] :

The following quantities of antigens were absorbed onto 96-well plates (Falcon 3072) : 2.5 µg of protein MalE, 5 µg of MalE-HspA, or 2.5 µg of MalE-HspB. The plates were left overnight at 4°C, then washed 3 times with ELISA wash solution (EWS) [1% PBS containing 0.05% (v/v) Tween 20]. Saturation was achieved by incubating the plates for 90 min at 37°C in EWS supplemented with 1% milk powder. Wells were again washed 3 times with EWS and then gently agitated for 90 min at 37°C in the presence of human sera (diluted 1:500 in EWS with 0.5% milk powder), under

agitation. Bound immunoglobulins were detected by incubation for 90 min at 37°C with biotinylated secondary antibody (goat anti-human IgG, IgA or IgM diluted [1:1000] in EWS supplemented with 0.5% milk powder) in combination with streptavidin-peroxidase (1:500) (Kirkegaard and Perry Lab.). Bound peroxidase was detected by reaction with the citrate substrate and hydrogen peroxide. Plates were incubated in the dark, at room temperature, and the optical density at 492 nm was read at intervals of 5, 15 and 30 min in an ELISA plate reader. After 30 min, the reaction was stopped by the addition of hydrochloric acid to a final concentration of 0.5M.

RESULTS OF PART IV EXPERIMENTS :

Construction of recombinant plasmids producing inducible MalE-HspA, and HspB fusion proteins :

The oligonucleotides #1 and #2 (hspA) and #3 and #4 (hspB) were used to amplify by PCR the entire hspA and the hspB genes, respectively. The PCR products were electroeluted, purified and restricted with EcoRI and PstI. The restricted fragments (360 bp and 1600 bp in size, respectively) were then ligated into the EcoRI-PstI restricted pMAL-c2 vector to generate plasmids designated pILL933 and pILL934, respectively. Following induction with IPTG, and purification of the soluble protein on amylose columns, fusion proteins of the expected size (55 kDa for pILL933 [figure 17], and 100 kDa for pILL934) were visualized on SDS-PAGE gels. Each of these corresponded to the fusion of the MalE protein (42.7 kDa) with the second amino-acid of each of the Hsp polypeptides. The yield of the expression of the fusion proteins was 100 mg for

MalE-HspA and 20 mg for MalE-HspB when prepared from 2 liters of broth culture.

Study of the antigenicity of the HspA and HspB fusion proteins, and of the immunogenicity of HspA and HspB in patients infected with *H. pylori* :

In order to determine whether the fusion proteins were still antigenic, each was analyzed by Western blot with rabbit antiserum raised against the MalE protein and a whole-cell extract of *H. pylori* strain 85P. Both fusion proteins were immunoreactive with antibody to MalE (not shown) and with the anti-*H. pylori* antiserum. The anti-*H. pylori* antiserum did not recognize the purified MalE protein (figure 18). These results demonstrated that the fusion proteins retained their antigenic properties ; in addition, whereas the HspB protein was known to be immunogenic, this is the first demonstration that HspA per se is immunogenic in rabbits.

In the same way, in order to determine whether the HspA and HspB polypeptides were immunogenic in humans, the humoral immune response against HspA and/or HspB in patients infected with *H. pylori* was analyzed and compared to that of uninfected persons using Western immunoblotting assays and enzyme-linked immunosorbent assays (ELISA). None of the 12 sera of the *H. pylori*-negative persons gave a positive immunoblot signal with MalE, MalE-HspA, or MalE-HspB proteins (figure 18). In contrast, of 28 sera from *H. pylori*-positive patients, 12 (42.8%) reacted with the HspA protein whilst 20 (71.4%) recognized the HspB protein. All of the sera that recognized HspA also reacted with the HspB protein. No association was observed between the immune response and the clinical presentation of the *H. pylori* infection although such

a conclusion might be premature because of the small number of strains analyzed.

Nickel binding properties of the fused MalE-HspA protein :

MBP-HspA recombinant protein expressed following induction with IPTG, was purified from a whole cell extract by one step purification on nickel affinity column whereas the MBP alone, nor MBP-HspB exhibited this property. Figure 18 illustrates the one step purification of the MBP-HspA protein that was eluted as a monomer at pH6.3, and as a monomer at pH4.5. The unique band seen in panel 7 and the two bands seen in panel 5 were both specifically recognized with anti-HspA rabbit sera. This suggested that the nickel binding property of the fused MBP-HspA protein might be attributed to the C-terminal sequence of HspA which is rich in Histidine and Cysteine residues.

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urease enzymes of Helicobacter species from
humans and animals. Infect Immun 60: 5259-5266.

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT:

(A) NAME: INSTITUT PASTEUR
(B) STREET: 25-28 rue du Dr Roux
(C) CITY: PARIS CEDEX 15
(E) COUNTRY: FRANCE
(F) POSTAL CODE (ZIP): 75724
(G) TELEPHONE: 45.68.80.94
(H) TELEFAX: 40.61.30.17

(A) NAME: INSTITUT NATIONAL DE LA SANTE ET DE LA
RECHERCHE MEDICALE
(B) STREET: 101 rue de Tolbiac
(C) CITY: PARIS CEDEX 13
(E) COUNTRY: FRANCE
(F) POSTAL CODE (ZIP): 75654
(G) TELEPHONE: 44.23.60.00
(H) TELEFAX: 45.85.07.66

(ii) TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS AGAINST
HELICOBACTER INFECTION, POLYPEPTIDES FOR USE IN THE
COMPOSITIONS AND NUCLEIC ACID SEQUENCES ENCODING SAID
POLYPEPTIDES.

(iii) NUMBER OF SEQUENCES: 8

(iv) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)

(v) CURRENT APPLICATION DATA:

APPLICATION NUMBER: EP 93401309.5

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2619 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION: 31..36
(D) OTHER INFORMATION: /standard_name= "Shine-Dalgarno
sequence"

83

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 756..759
- (D) OTHER INFORMATION: /standard_name= "Shine-Dalgarno sequence"

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 43..753
- (D) OTHER INFORMATION: /standard_name= "URE A"

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 766..2475
- (D) OTHER INFORMATION: /standard_name= "URE B"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

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GAA GAA CGC TTG GCG CGT GGT GTG AAA CTC AAT TAC ACC GAA GCG GTC Glu Glu Arg Leu Ala Arg Gly Val Lys Leu Asn Tyr Thr Glu Ala Val 25 30 35	150
GCG CTC ATT AGC GGG CGT GTG ATG GAA AAG GCG CGT GAT GGT AAT AAA Ala Leu Ile Ser Gly Arg Val Met Glu Lys Ala Arg Asp Gly Asn Lys 40 45 50	198
AGC GTG GCG GAT TTG ATG CAA GAA GGC AGG ACT TGG CTT AAA AAA GAA Ser Val Ala Asp Leu Met Gln Glu Gly Arg Thr Trp Leu Lys Lys Glu 55 60 65	246
AAT GTG ATG GAC GGC GTA GCA AGC ATG ATT CAT GAA GTG GGC ATT GAA Asn Val Met Asp Gly Val Ala Ser Met Ile His Glu Val Gly Ile Glu 70 75 80	294
GCT AAC TTC CCC GAT GGA ACC AAG CTT GTA ACT ATC CAC ACT CCG GTA Ala Asn Phe Pro Asp Gly Thr Lys Leu Val Thr Ile His Thr Pro Val 85 90 95 100	342
GAG GAT AAT GGC AAA TTA GCC CCC GGC GAG GTC TTC TTA AAA AAT GAG Glu Asp Asn Gly Lys Leu Ala Pro Gly Glu Val Phe Leu Lys Asn Glu 105 110 115	390
GAC ATT ACT ATT AAC GCC GGC AAA GAA GCC ATT AGC TTG AAA GTG AAA Asp Ile Thr Ile Asn Ala Gly Lys Glu Ala Ile Ser Leu Lys Val Lys 120 125 130	438

84																
AAT	AAA	GGC	GAT	CGT	CCT	GTG	CAG	GTG	GGA	TCA	CAT	TTC	CAC	TTC	TTC	486
Asn	Lys	Gly	Asp	Arg	Pro	Val	Gln	Val	Gly	Ser	His	Phe	His	Phe	Phe	
135						140			145							
GAA	GTG	AAT	AAG	CTC	TTG	GAC	TTC	GAT	CGC	GCA	AAA	AGC	TTT	TGC	AAA	534
Glu	Val	Asn	Lys	Leu	Leu	Asp	Phe	Asp	Arg	Ala	Lys	Ser	Phe	Cys	Lys	
150						155			160							
CGC	CTA	GAC	ATT	GCA	TCT	GGA	ACA	GCG	GTG	CGC	TTT	GAA	CCC	GGG	GAG	582
Arg	Leu	Asp	Ile	Ala	Ser	Gly	Thr	Ala	Val	Arg	Phe	Glu	Pro	Gly	Glu	
165				170			175						180			
GAA	AAA	AGT	GTG	GAA	CTC	ATT	GAC	ATC	GGC	GGG	AAT	AAG	CGC	ATC	TAT	630
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185						190						195				
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Gly	Phe	Asn	Ser	Leu	Val	Asp	Arg	Gln	Ala	Asp	Ala	Asp	Gly	Lys	Lys	
200						205						210				
CTC	GGC	TTA	AAA	CGC	GCT	AAA	GAA	AAA	GGT	TTT	GGG	TCT	GTA	AAC	TGC	726
Leu	Gly	Leu	Lys	Arg	Ala	Lys	Glu	Lys	Gly	Phe	Gly	Ser	Val	Asn	Cys	
215						220						225				
GGT	TGT	GAA	GCG	ACT	AAA	GAT	AAA	CAA	TAAGGAAAAA	CC	ATG	AAA	AAG			774
Gly	Cys	Glu	Ala	Thr	Lys	Asp	Lys	Gln				Met	Lys	Lys		
230						235						1				
ATT	TCA	CGA	AAA	GAA	TAT	GTT	TCT	ATG	TAT	GGT	CCC	ACT	ACC	GGG	GAT	822
Ile	Ser	Arg	Lys	Glu	Tyr	Val	Ser	Met	Tyr	Gly	Pro	Thr	Thr	Gly	Asp	
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CGT	GTT	AGA	CTC	GGC	GAC	ACT	GAT	TTG	ATC	TTA	GAA	GTG	GAG	CAT	GAT	870
Arg	Val	Arg	Leu	Gly	Asp	Thr	Asp	Leu	Ile	Leu	Glu	Val	Glu	His	Asp	
20						25						30			35	
TGC	ACC	ACT	TAT	GGT	GAA	GAG	ATC	AAA	TTT	GGG	GGC	GGT	AAA	ACT	ATC	918
Cys	Thr	Thr	Tyr	Gly	Glu	Glu	Ile	Lys	Phe	Gly	Gly	Gly	Lys	Thr	Ile	
			40						45						50	
CGT	GAT	GGG	ATG	AGT	CAA	ACC	AAT	AGC	CCT	AGC	TCT	TAT	GAA	TTA	GAT	966
Arg	Asp	Gly	Met	Ser	Gln	Thr	Asn	Ser	Pro	Ser	Ser	Tyr	Glu	Leu	Asp	
			55						60						65	
TTG	GTG	CTC	ACT	AAC	GCC	CTC	ATT	GTG	GAC	TAT	ACG	GGC	ATT	TAC	AAA	1014
Leu	Val	Leu	Thr	Asn	Ala	Leu	Ile	Val	Asp	Tyr	Thr	Gly	Ile	Tyr	Lys	
70						75						80				
GCC	GAC	ATT	GGG	ATT	AAA	GAC	GGC	AAG	ATT	GCA	GGC	ATT	GGC	AAG	GCA	1062
Ala	Asp	Ile	Gly	Ile	Lys	Asp	Gly	Lys	Ile	Ala	Gly	Ile	Gly	Lys	Ala	
85						90						95				
GGC	AAT	AAG	GAC	ATG	CAA	GAT	GGC	GTA	GAT	AAT	AAT	CTT	TGC	GTA	GGT	1110
Gly	Asn	Lys	Asp	Met	Gln	Asp	Gly	Val	Asp	Asn	Asn	Leu	Cys	Val	Gly	

85

CCT GCT ACA GAG GCT TTG GCA GCT GAG GGC TTG ATT GTA ACC GCT GGT Pro Ala Thr Glu Ala Leu Ala Ala Glu Gly Leu Ile Val Thr Ala Gly 120 125 130	1158
GGC ATC GAT ACG CAT ATT CAC TTT ATC TCT CCC CAA CAA ATC CCT ACT Gly Ile Asp Thr His Ile His Phe Ile Ser Pro Gln Gln Ile Pro Thr 135 140 145	1206
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AAA AGT ATG TTG CGT GCA GCC GAA GAA TAC GCC ATG AAT CTA GGC TTT Lys Ser Met Leu Arg Ala Ala Glu Glu Tyr Ala Met Asn Leu Gly Phe 180 185 190 195	1350
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CCT GCA GCT ATT CAC CAC TGC CTC AAT GTC GCC GAT GAA TAC GAT GTG Pro Ala Ala Ile His His Cys Leu Asn Val Ala Asp Glu Tyr Asp Val 230 235 240	1494
CAA GTG GCT ATC CAC ACC GAT ACC CTT AAC GAG GCG GGC TGT GTA GAA Gln Val Ala Ile His Thr Asp Thr Leu Asn Glu Ala Gly Cys Val Glu 245 250 255	1542
GAC ACC CTA GAG GCG ATT GCC GGG CGC ACC ATC CAT ACC TTC CAC ACT Asp Thr Leu Glu Ala Ile Ala Gly Arg Thr Ile His Thr Phe His Thr 260 265 270 275	1590
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86

CGC	CCC	CAA	ACT	ATC	GCG	GCT	GAA	GAC	CAA	CTC	CAT	GAC	ATG	GGG	ATC	1830
Arg	Pro	Gln	Thr	Ile	Ala	Ala	Glu	Asp	Gln	Leu	His	Asp	Met	Gly	Ile	
340					345				350					355		
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Phe	Ser	Ile	Thr	Ser	Ser	Asp	Ser	Gln	Ala	Met	Gly	Arg	Val	Gly	Glu	
				360				365						370		
GTG	ATC	ACA	CGC	ACT	TGG	CAG	ACA	GCA	GAC	AAA	AAC	AAA	AAA	GAG	TTT	1926
Val	Ile	Thr	Arg	Thr	Trp	Gln	Thr	Ala	Asp	Lys	Asn	Lys	Lys	Glu	Phe	
			375					380						385		
GGG	CGC	TTG	AAA	GAG	GAA	AAA	GGC	GAT	AAC	GAC	AAC	TTC	CGC	ATC	AAA	1974
Gly	Arg	Leu	Lys	Glu	Glu	Lys	Gly	Asp	Asn	Asp	Asn	Phe	Arg	Ile	Lys	
		390					395					400				
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Arg	Tyr	Ile	Ser	Lys	Tyr	Thr	Ile	Asn	Pro	Gly	Ile	Ala	His	Gly	Ile	
	405					410					415					
TCT	GAC	TAT	GTG	GGC	TCT	GTG	GAA	GTG	GGC	AAA	TAC	GCC	GAC	CTC	GTG	2070
Ser	Asp	Tyr	Val	Gly	Ser	Val	Glu	Val	Gly	Lys	Tyr	Ala	Asp	Leu	Val	
420					425					430				435		
CTT	TGG	AGT	CCG	GCT	TTC	TTT	GGC	ATT	AAG	CCC	AAT	ATG	ATT	ATT	AAG	2118
Leu	Trp	Ser	Pro	Ala	Phe	Phe	Gly	Ile	Lys	Pro	Asn	Met	Ile	Ile	Lys	
				440					445					450		
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Gly	Gly	Phe	Ile	Ala	Leu	Ser	Gln	Met	Gly	Asp	Ala	Asn	Ala	Ser	Ile	
			455					460					465			
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Pro	Thr	Pro	Gln	Pro	Val	Tyr	Tyr	Arg	Glu	Met	Phe	Gly	His	His	Gly	
		470					475					480				
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Lys	Asn	Lys	Phe	Asp	Thr	Asn	Ile	Thr	Phe	Val	Ser	Gln	Ala	Ala	Tyr	
	485					490					495					
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Lys	Ala	Gly	Ile	Lys	Glu	Glu	Leu	Gly	Leu	Asp	Arg	Ala	Ala	Pro	Pro	
500					505				510					515		
GTG	AAA	AAC	TGT	CGC	AAT	ATC	ACT	AAA	AAG	GAC	CTC	AAA	TTC	AAC	GAT	2358
Val	Lys	Asn	Cys	Arg	Asn	Ile	Thr	Lys	Lys	Asp	Leu	Lys	Phe	Asn	Asp	
				520					525					530		
GTG	ACC	GCA	CAT	ATT	GAT	GTC	AAC	CCT	GAA	ACC	TAT	AAG	GTG	AAA	GTG	2406
Val	Thr	Ala	His	Ile	Asp	Val	Asn	Pro	Glu	Thr	Tyr	Lys	Val	Lys	Val	
			535					540					545			
GAT	GGC	AAA	GAG	GTA	ACC	TCT	AAA	GCA	GCA	GAT	GAA	TTG	AGC	CTA	GCG	2454
Asp	Gly	Lys	Glu	Val	Thr	Ser	Lys	Ala	Ala	Asp	Glu	Leu	Ser	Leu	Ala	
		550					555					560				

87

CAA CTT TAT AAT TTG TTC TAGGAGGCTA AGGAGGGGGA TAGAGGGGGT 2502
 Gln Leu Tyr Asn Leu Phe
 565 570

TTATTTAGAG GGGAGTCATT GATTTACCTT TGCTAGTTTA TAATGGATTT AAGAGAGGTT 2562

TTTTTTCGTG TTTTATACCG CGTTGAAACC CTCAAATCTT TACCAAAAGG ATGCTAA 2619

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 237 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter felis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Met	Lys	Leu	Thr	Pro	Lys	Glu	Leu	Asp	Lys	Leu	Met	Leu	His	Tyr	Ala	
1				5					10					15		
Gly	Arg	Leu	Ala	Glu	Glu	Arg	Leu	Ala	Arg	Gly	Val	Lys	Leu	Asn	Tyr	
			20					25					30			
Thr	Glu	Ala	Val	Ala	Leu	Ile	Ser	Gly	Arg	Val	Met	Glu	Lys	Ala	Arg	
			35				40					45				
Asp	Gly	Asn	Lys	Ser	Val	Ala	Asp	Leu	Met	Gln	Glu	Gly	Arg	Thr	Trp	
	50					55				60						
Leu	Lys	Lys	Glu	Asn	Val	Met	Asp	Gly	Val	Ala	Ser	Met	Ile	His	Glu	
65				70					75					80		
Val	Gly	Ile	Glu	Ala	Asn	Phe	Pro	Asp	Gly	Thr	Lys	Leu	Val	Thr	Ile	
			85					90					95			
His	Thr	Pro	Val	Glu	Asp	Asn	Gly	Lys	Leu	Ala	Pro	Gly	Glu	Val	Phe	
			100				105					110				
Leu	Lys	Asn	Glu	Asp	Ile	Thr	Ile	Asn	Ala	Gly	Lys	Glu	Ala	Ile	Ser	
	115					120					125					
Leu	Lys	Val	Lys	Asn	Lys	Gly	Asp	Arg	Pro	Val	Gln	Val	Gly	Ser	His	
	130				135					140						
Phe	His	Phe	Phe	Glu	Val	Asn	Lys	Leu	Leu	Asp	Phe	Asp	Arg	Ala	Lys	
145				150					155					160		
Ser	Phe	Cys	Lys	Arg	Leu	Asp	Ile	Ala	Ser	Gly	Thr	Ala	Val	Arg	Phe	
			165				170						175			

88

Glu Pro Gly Glu Glu Lys Ser Val Glu Leu Ile Asp Ile Gly Gly Asn
 180 185 190

Lys Arg Ile Tyr Gly Phe Asn Ser Leu Val Asp Arg Gln Ala Asp Ala
 195 200 205

Asp Gly Lys Lys Leu Gly Leu Lys Arg Ala Lys Glu Lys Gly Phe Gly
 210 215 220

Ser Val Asn Cys Gly Cys Glu Ala Thr Lys Asp Lys Gln
 225 230 235

(2) INFORMATION FOR SEQ ID NO: 3:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 569 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE :

(A) ORGANISM: *Helicobacter felis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

Met Lys Lys Ile Ser Arg Lys Glu Tyr Val Ser Met Tyr Gly Pro Thr
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Thr Gly Asp Arg Val Arg Leu Gly Asp Thr Asp Leu Ile Leu Glu Val
 20 25 30

Glu His Asp Cys Thr Thr Tyr Gly Glu Glu Ile Lys Phe Gly Gly Gly
 35 40 45

Lys Thr Ile Arg Asp Gly Met Ser Gln Thr Asn Ser Pro Ser Ser Tyr
 50 55 60

Glu Leu Asp Leu Val Leu Thr Asn Ala Leu Ile Val Asp Tyr Thr Gly
 65 70 75 80

Ile Tyr Lys Ala Asp Ile Gly Ile Lys Asp Gly Lys Ile Ala Gly Ile
 85 90 95

Gly Lys Ala Gly Asn Lys Asp Met Gln Asp Gly Val Asp Asn Asn Leu
 100 105 110

Cys Val Gly Pro Ala Thr Glu Ala Leu Ala Ala Glu Gly Leu Ile Val
 115 120 125

Thr Ala Gly Gly Ile Asp Thr His Ile His Phe Ile Ser Pro Gln Gln
 130 135 140

Ile Pro Thr Ala Phe Ala Ser Gly Val Thr Thr Met Ile Gly Gly Gly
 145 150 155 160

89

Thr Gly Pro Ala Asp Gly Thr Asn Ala Thr Thr Ile Thr Pro Gly Arg
 165 170 175
 Ala Asn Leu Lys Ser Met Leu Arg Ala Ala Glu Glu Tyr Ala Met Asn
 180 185 190
 Leu Gly Phe Leu Ala Lys Gly Asn Val Ser Tyr Glu Pro Ser Leu Arg
 195 200 205
 Asp Gln Ile Glu Ala Gly Ala Ile Gly Phe Lys Ile His Glu Asp Trp
 210 215 220
 Gly Ser Thr Pro Ala Ala Ile His His Cys Leu Asn Val Ala Asp Glu
 225 230 235 240
 Tyr Asp Val Gln Val Ala Ile His Thr Asp Thr Leu Asn Glu Ala Gly
 245 250 255
 Cys Val Glu Asp Thr Leu Glu Ala Ile Ala Gly Arg Thr Ile His Thr
 260 265 270
 Phe His Thr Glu Gly Ala Gly Gly Gly His Ala Pro Asp Val Ile Lys
 275 280 285
 Met Ala Gly Glu Phe Asn Ile Leu Pro Ala Ser Thr Asn Pro Thr Ile
 290 295 300
 Pro Phe Thr Lys Asn Thr Glu Ala Glu His Met Asp Met Leu Met Val
 305 310 315 320
 Cys His His Leu Asp Lys Ser Ile Lys Glu Asp Val Gln Phe Ala Asp
 325 330 335
 Ser Arg Ile Arg Pro Gln Thr Ile Ala Ala Glu Asp Gln Leu His Asp
 340 345 350
 Met Gly Ile Phe Ser Ile Thr Ser Ser Asp Ser Gln Ala Met Gly Arg
 355 360 365
 Val Gly Glu Val Ile Thr Arg Thr Trp Gln Thr Ala Asp Lys Asn Lys
 370 375 380
 Lys Glu Phe Gly Arg Leu Lys Glu Glu Lys Gly Asp Asn Asp Asn Phe
 385 390 395 400
 Arg Ile Lys Arg Tyr Ile Ser Lys Tyr Thr Ile Asn Pro Gly Ile Ala
 405 410 415
 His Gly Ile Ser Asp Tyr Val Gly Ser Val Glu Val Gly Lys Tyr Ala
 420 425 430
 Asp Leu Val Leu Trp Ser Pro Ala Phe Phe Gly Ile Lys Pro Asn Met
 435 440 445
 Ile Ile Lys Gly Gly Phe Ile Ala Leu Ser Gln Met Gly Asp Ala Asn
 450 455 460

90

Ala Ser Ile Pro Thr Pro Gln Pro Val Tyr Tyr Arg Glu Met Phe Gly
465 470 475 480

His His Gly Lys Asn Lys Phe Asp Thr Asn Ile Thr Phe Val Ser Gln
485 490 495

Ala Ala Tyr Lys Ala Gly Ile Lys Glu Glu Leu Gly Leu Asp Arg Ala
500 505 510

Ala Pro Pro Val Lys Asn Cys Arg Asn Ile Thr Lys Lys Asp Leu Lys
515 520 525

Phe Asn Asp Val Thr Ala His Ile Asp Val Asn Pro Glu Thr Tyr Lys
530 535 540

Val Lys Val Asp Gly Lys Glu Val Thr Ser Lys Ala Ala Asp Glu Leu
545 550 555 560

Ser Leu Ala Gln Leu Tyr Asn Leu Phe
565

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2284 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 124..477
- (D) OTHER INFORMATION: /standard_name= "H. pylori - Hsp A"

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 506..2143
- (D) OTHER INFORMATION: /standard_name= "H. pylori - Hsp B"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

ACAAACATGA TCTCATATCA GGGACTTGTT CGCACCTTCC CTAAAAATGC GCTATAGTTG 60

TGTCGCTTAA GAATACTAAG CGCTAAATTT CTATTTTATT TATCAAAACT TAGGAGAACT 120

GAA ATG AAG TTT CAA CCA TTA GGA GAA AGG GTC TTA GTA GAA AGA CTT 168
Met Lys Phe Gln Pro Leu Gly Glu Arg Val Leu Val Glu Arg Leu
1 5 10 15

GAA GAA GAG AAC AAA ACC AGT TCA GGC ATC ATC ATC CCT GAT AAC GCT 216
Glu Glu Glu Asn Lys Thr Ser Ser Gly Ile Ile Ile Pro Asp Asn Ala
20 25 30

91

AAA GAA AAG CCT TTA ATG GGC GTA GTC AAA GCG GTT AGC CAT AAA ATC	264
Lys Glu Lys Pro Leu Met Gly Val Val Lys Ala Val Ser His Lys Ile	
35 40 45	
AGT GAG GGT TGC AAA TGC GTT AAA GAA GGC GAT GTG ATC GCT TTT GGC	312
Ser Glu Gly Cys Lys Cys Val Lys Glu Gly Asp Val Ile Ala Phe Gly	
50 55 60	
AAA TAC AAA GGC GCA GAA ATC GTT TTA GAT GGC GTT GAA TAC ATG GTG	360
Lys Tyr Lys Gly Ala Glu Ile Val Leu Asp Gly Val Glu Tyr Met Val	
65 70 75	
CTA GAA CTA GAA GAC ATT CTA GGT ATT GTG GGC TCA GGC TCT TGC TGT	408
Leu Glu Leu Glu Asp Ile Leu Gly Ile Val Gly Ser Gly Ser Cys Cys	
80 85 90 95	
CAT ACA GGT AAT CAT GAT CAT AAA CAT GCT AAA GAG CAT GAA GCT TGC	456
His Thr Gly Asn His Asp His Lys His Ala Lys Glu His Glu Ala Cys	
100 105 110	
TGT CAT GAT CAC AAA AAA CAC TAAAAAACAT TATTATTAAG GATACAAA ATG	508
Cys His Asp His Lys Lys His Met	
115 1	
GCA AAA GAA ATC AAA TTT TCA GAT AGC GCA AGA AAC CTT TTA TTT GAA	556
Ala Lys Glu Ile Lys Phe Ser Asp Ser Ala Arg Asn Leu Leu Phe Glu	
5 10 15	
GGC GTA AGA CAA CTC CAT GAC GCT GTC AAA GTA ACC ATG GGG CCA AGA	604
Gly Val Arg Gln Leu His Asp Ala Val Lys Val Thr Met Gly Pro Arg	
20 25 30	
GGC AGG AAC GTG TTG ATC CAA AAA AGC TAT GGC GCT CCA AGC ATC ACC	652
Gly Arg Asn Val Leu Ile Gln Lys Ser Tyr Gly Ala Pro Ser Ile Thr	
35 40 45	
AAA GAC GGC GTG AGC GTG GCT AAA GAG ATT GAA TTA AGT TGC CCC GTG	700
Lys Asp Gly Val Ser Val Ala Lys Glu Ile Glu Leu Ser Cys Pro Val	
50 55 60 65	
GCT AAC ATG GGC GCT CAG CTC GTT AAA GAA GAT GCG AGC AAA ACC GCT	748
Ala Asn Met Gly Ala Gln Leu Val Lys Glu Asp Ala Ser Lys Thr Ala	
70 75 80	
GAT GCC GCC GGC GAT GGC ACG ACC ACA GCG ACC GTG CTG GCT TAT AGC	796
Asp Ala Ala Gly Asp Gly Thr Thr Thr Ala Thr Val Leu Ala Tyr Ser	
85 90 95	
ATT TTT AAA GAG GGC TTG AGG AAT ATC ACG GCT GGG GCT AAC CCT ATT	844
Ile Phe Lys Glu Gly Leu Arg Asn Ile Thr Ala Gly Ala Asn Pro Ile	
100 105 110	
GAA GTG AAA CGA GGC ATG GAT AAA GCG CCT GAA GCG ATC ATT AAT GAG	892
Glu Val Lys Arg Gly Met Asp Lys Ala Pro Glu Ala Ile Ile Asn Glu	
115 120 125	

92

CTT AAA AAA GCG AGC AAA AAA GTG GGC GGT AAA GAA GAA ATC ACC CAA Leu Lys Lys Ala Ser Lys Lys Val Gly Gly Lys Glu Glu Ile Thr Gln 130 135 140 145	940
GTA GCG ACC ATT TCT GCA AAC TCC GAT CAC AAT ATC GGG AAA CTC ATC Val Ala Thr Ile Ser Ala Asn Ser Asp His Asn Ile Gly Lys Leu Ile 150 155 160	988
GCT GAC GCT ATG GAA AAA GTG GGT AAA GAC GGC GTG ATC ACC GTT GAA Ala Asp Ala Met Glu Lys Val Gly Lys Asp Gly Val Ile Thr Val Glu 165 170 175	1036
GAA GCT AAG GGC ATT GAA GAT GAA TTA GAT GTC GTA GAA GGC ATG CAA Glu Ala Lys Gly Ile Glu Asp Glu Leu Asp Val Val Glu Gly Met Gln 180 185 190	1084
TTT GAT AGA GGC TAC CTC TCC CCT TAC TTT GTA ACC AAC GCT GAG AAA Phe Asp Arg Gly Tyr Leu Ser Pro Tyr Phe Val Thr Asn Ala Glu Lys 195 200 205	1132
ATG ACC GCT CAA TTG GAT AAC GCT TAC ATC CTT TTA ACG GAT AAA AAA Met Thr Ala Gln Leu Asp Asn Ala Tyr Ile Leu Leu Thr Asp Lys Lys 210 215 220 225	1180
ATC TCT AGC ATG AAA GAC ATT CTC CCG CTA CTA GAA AAA ACC ATG AAA Ile Ser Ser Met Lys Asp Ile Leu Pro Leu Leu Glu Lys Thr Met Lys 230 235 240	1228
GAG GGC AAA CCG CTT TTA ATC ATC GCT GAA GAC ATT GAG GGC GAA GCT Glu Gly Lys Pro Leu Leu Ile Ile Ala Glu Asp Ile Glu Gly Glu Ala 245 250 255	1276
TTA ACG ACT CTA GTG GTG AAT AAA TTA AGA GGC GTG TTG AAT ATC GCA Leu Thr Thr Leu Val Val Asn Lys Leu Arg Gly Val Leu Asn Ile Ala 260 265 270	1324
GCG GTT AAA GCT CCA GGC TTT GGG GAC AGG AGA AAA GAA ATG CTC AAA Ala Val Lys Ala Pro Gly Phe Gly Asp Arg Arg Lys Glu Met Leu Lys 275 280 285	1372
GAC ATC GCT GTT TTA ACC GGC GGT CAA GTC ATT AGC GAA GAA TTG GGC Asp Ile Ala Val Leu Thr Gly Gly Gln Val Ile Ser Glu Glu Leu Gly 290 295 300 305	1420
TTG AGT CTA GAA AAC GCT GAA GTG GAG TTT TTA GGC AAA GCG AAG ATT Leu Ser Leu Glu Asn Ala Glu Val Glu Phe Leu Gly Lys Ala Lys Ile 310 315 320	1468
GTG ATT GAC AAA GAC AAC ACC ACG ATC GTA GAT GGC AAA GGC CAT AGC Val Ile Asp Lys Asp Asn Thr Thr Ile Val Asp Gly Lys Gly His Ser 325 330 335	1516
CAT GAC GTC AAA GAC AGA GTC GCG CAA ATC AAA ACC CAA ATT GCA AGC His Asp Val Lys Asp Arg Val Ala Gln Ile Lys Thr Gln Ile Ala Ser 340 345 350	1564

93

ACG Thr	ACA Thr	AGC Ser	GAT Asp	TAC Tyr	GAC Asp	AAA Lys	GAA Glu	AAA Lys	TTG Leu	CAA Gln	GAA Glu	AGA Arg	TTG Leu	GCC Ala	AAA Lys	1612
355 360 365																
CTC Leu	TCT Ser	GGC Gly	GGT Gly	GTG Val	GCT Ala	GTG Val	ATT Ile	AAA Lys	GTG Val	GGC Gly	GCT Ala	CCG Ala	AGT Ser	GAA Glu	GTG Val	1660
370 375 380 385																
GAA Glu	ATG Met	AAA Lys	GAG Glu	AAA Lys	AAA Lys	GAC Asp	CGG Arg	GTG Val	GAT Asp	GAC Asp	CCG Ala	TTG Leu	AGC Ser	CCG Ala	ACT Thr	1708
390 395 400																
AAA Lys	CGC Ala	CGC Ala	GTT Val	GAA Glu	GAA Glu	GGC Gly	ATT Ile	GTG Val	ATT Ile	GGG Gly	GGC Gly	GGT Gly	CCG Ala	GCC Ala	CTC Leu	1756
405 410 415																
ATT Ile	CGC Arg	CGC Ala	GCC Ala	CAA Gln	AAA Lys	GTG Val	CAT His	TTG Leu	AAT Asn	TTA Leu	CAC His	GAT Asp	GAT Asp	GAA Glu	AAA Lys	1804
420 425 430																
GTG Val	GGC Gly	TAT Tyr	GAA Glu	ATC Ile	ATC Ile	ATG Met	CGC Arg	GCC Ala	ATT Ile	AAA Lys	GCC Ala	CCA Pro	TTA Leu	GCT Ala	CAA Gln	1852
435 440 445																
ATC Ile	GCT Ala	ATC Ile	AAT Asn	GCC Ala	GGT Gly	TAT Tyr	GAT Asp	GGC Gly	GGT Gly	GTG Val	GTC Val	GTG Val	AAT Asn	GAA Glu	GTA Val	1900
450 455 460 465																
GAA Glu	AAA Lys	CAC His	GAA Glu	GGG Gly	CAT His	TTT Phe	GGT Gly	TTT Phe	AAC Asn	GCT Ala	AGC Ser	AAT Asn	GGC Gly	AAG Lys	TAT Tyr	1948
470 475 480																
GTG Val	GAC Asp	ATG Met	TTT Phe	AAA Lys	GAA Glu	GGC Gly	ATT Ile	ATT Ile	GAC Asp	CCC Pro	TTA Leu	AAA Lys	GTA Val	GAA Glu	AGG Arg	1996
485 490 495																
ATC Ile	GCT Ala	TTA Leu	CAA Gln	AAT Asn	GCG Ala	GTT Val	TCG Ser	GTT Val	TCA Ser	AGC Ser	CTG Leu	CTT Leu	TTA Leu	ACC Thr	ACA Thr	2044
500 505 510																
GAA Glu	GCC Ala	ACC Thr	GTG Val	CAT His	GAA Glu	ATC Ile	AAA Lys	GAA Glu	GAA Glu	AAA Lys	GCG Ala	GCC Ala	CCA Pro	GCA Ala	ATG Met	2092
515 520 525																
CCT Pro	GAT Asp	ATG Met	GGT Gly	GGC Gly	ATG Met	GGC Gly	GGA Gly	ATG Met	GGA Gly	GGC Gly	ATG Met	GGC Gly	GGC Gly	ATG Met	ATG Met	2140
530 535 540 545																
TAAGCCCCCT TGCTTTTTTG TATCATCTGC TTTTAAATC CATCTTCTAG AATCCCCCCT 2200																
TCTAAATCC CTTTTTTGGG GGGTGCTTTT GGTTTGATAA AACCGCTCGC TTTTAAAAAC 2260																
GCGCAACAAA AAACCTCTGTT AAGC 2284																

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 545 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

(A) ORGANISM : H. pylori

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

```

Met Ala Lys Glu Ile Lys Phe Ser Asp Ser Ala Arg Asn Leu Leu Phe
 1             5             10             15
Glu Gly Val Arg Gln Leu His Asp Ala Val Lys Val Thr Met Gly Pro
      20             25             30
Arg Gly Arg Asn Val Leu Ile Gln Lys Ser Tyr Gly Ala Pro Ser Ile
      35             40             45
Thr Lys Asp Gly Val Ser Val Ala Lys Glu Ile Glu Leu Ser Cys Pro
      50             55             60
Val Ala Asn Met Gly Ala Gln Leu Val Lys Glu Asp Ala Ser Lys Thr
      65             70             75             80
Ala Asp Ala Ala Gly Asp Gly Thr Thr Thr Ala Thr Val Leu Ala Tyr
      85             90             95
Ser Ile Phe Lys Glu Gly Leu Arg Asn Ile Thr Ala Gly Ala Asn Pro
      100            105            110
Ile Glu Val Lys Arg Gly Met Asp Lys Ala Pro Glu Ala Ile Ile Asn
      115            120            125
Glu Leu Lys Lys Ala Ser Lys Lys Val Gly Gly Lys Glu Glu Ile Thr
      130            135            140
Gln Val Ala Thr Ile Ser Ala Asn Ser Asp His Asn Ile Gly Lys Leu
      145            150            155            160
Ile Ala Asp Ala Met Glu Lys Val Gly Lys Asp Gly Val Ile Thr Val
      165            170            175
Glu Glu Ala Lys Gly Ile Glu Asp Glu Leu Asp Val Val Glu Gly Met
      180            185            190
Gln Phe Asp Arg Gly Tyr Leu Ser Pro Tyr Phe Val Thr Asn Ala Glu
      195            200            205
Lys Met Thr Ala Gln Leu Asp Asn Ala Tyr Ile Leu Leu Thr Asp Lys
      210            215            220

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95

Lys Ile Ser Ser Met Lys Asp Ile Leu Pro Leu Leu Glu Lys Thr Met
 225 230 235 240
 Lys Glu Gly Lys Pro Leu Leu Ile Ile Ala Glu Asp Ile Glu Gly Glu
 245 250 255
 Ala Leu Thr Thr Leu Val Val Asn Lys Leu Arg Gly Val Leu Asn Ile
 260 265 270
 Ala Ala Val Lys Ala Pro Gly Phe Gly Asp Arg Arg Lys Glu Met Leu
 275 280 285
 Lys Asp Ile Ala Val Leu Thr Gly Gly Gln Val Ile Ser Glu Glu Leu
 290 295 300
 Gly Leu Ser Leu Glu Asn Ala Glu Val Glu Phe Leu Gly Lys Ala Lys
 305 310 315 320
 Ile Val Ile Asp Lys Asp Asn Thr Thr Ile Val Asp Gly Lys Gly His
 325 330 335
 Ser His Asp Val Lys Asp Arg Val Ala Gln Ile Lys Thr Gln Ile Ala
 340 345 350
 Ser Thr Thr Ser Asp Tyr Asp Lys Glu Lys Leu Gln Glu Arg Leu Ala
 355 360 365
 Lys Leu Ser Gly Gly Val Ala Val Ile Lys Val Gly Ala Ala Ser Glu
 370 375 380
 Val Glu Met Lys Glu Lys Lys Asp Arg Val Asp Asp Ala Leu Ser Ala
 385 390 395 400
 Thr Lys Ala Ala Val Glu Glu Gly Ile Val Ile Gly Gly Gly Ala Ala
 405 410 415
 Leu Ile Arg Ala Ala Gln Lys Val His Leu Asn Leu His Asp Asp Glu
 420 425 430
 Lys Val Gly Tyr Glu Ile Ile Met Arg Ala Ile Lys Ala Pro Leu Ala
 435 440 445
 Gln Ile Ala Ile Asn Ala Gly Tyr Asp Gly Gly Val Val Val Asn Glu
 450 455 460
 Val Glu Lys His Glu Gly His Phe Gly Phe Asn Ala Ser Asn Gly Lys
 465 470 475 480
 Tyr Val Asp Met Phe Lys Glu Gly Ile Ile Asp Pro Leu Lys Val Glu
 485 490 495
 Arg Ile Ala Leu Gln Asn Ala Val Ser Val Ser Ser Leu Leu Leu Thr
 500 505 510
 Thr Glu Ala Thr Val His Glu Ile Lys Glu Glu Lys Ala Ala Pro Ala
 515 520 525

96

Met Pro Asp Met Gly Gly Met Gly Gly Met Gly Gly Met Gly Gly Met
 530 535 540

Met
 545

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 118 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

- (A) ORGANISM : H. pylori

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

Met Lys Phe Gln Pro Leu Gly Glu Arg Val Leu Val Glu Arg Leu Glu
 1 5 10 15
 Glu Glu Asn Lys Thr Ser Ser Gly Ile Ile Ile Pro Asp Asn Ala Lys
 20 25 30
 Glu Lys Pro Leu Met Gly Val Val Lys Ala Val Ser His Lys Ile Ser
 35 40 45
 Glu Gly Cys Lys Cys Val Lys Glu Gly Asp Val Ile Ala Phe Gly Lys
 50 55 60
 Tyr Lys Gly Ala Glu Ile Val Leu Asp Gly Val Glu Tyr Met Val Leu
 65 70 75 80
 Glu Leu Glu Asp Ile Leu Gly Ile Val Gly Ser Gly Ser Cys Cys His
 85 90 95
 Thr Gly Asn His Asp His Lys His Ala Lys Glu His Glu Ala Cys Cys
 100 105 110
 His Asp His Lys Lys His
 115

(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 591 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM : H. felis

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..591

(D) OTHER INFORMATION: /standard_name= "URE I"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

ATG TTA GGT CTT GTG TTA TTG TAT GTT GCG GTC GTG CTG ATC AGC AAC	48
Met Leu Gly Leu Val Leu Leu Tyr Val Ala Val Val Leu Ile Ser Asn	
1 5 10 15	
GGA GTT AGT GGG CTT GCA AAT GTG GAT GCC AAA AGC AAA GCC ATC ATG	96
Gly Val Ser Gly Leu Ala Asn Val Asp Ala Lys Ser Lys Ala Ile Met	
20 25 30	
AAC TAC TTT GTG GGG GGG GAC TCT CCA TTG TGT GTA ATG TGG TCG CTA	144
Asn Tyr Phe Val Gly Gly Asp Ser Pro Leu Cys Val Met Trp Ser Leu	
35 40 45	
TCA TCT TAT TCC ACT TTC CAC CCC ACC CCC CCT GCA ACT GGT CCA GAA	192
Ser Ser Tyr Ser Thr Phe His Pro Thr Pro Pro Ala Thr Gly Pro Glu	
50 55 60	
GAT GTC GCG CAG GTG TCT CAA CAC CTC ATT AAC TTC TAT GGT CCA GCG	240
Asp Val Ala Gln Val Ser Gln His Leu Ile Asn Phe Tyr Gly Pro Ala	
65 70 75 80	
ACT GGT CTA TTG TTT GGT TTT ACC TAC TTG TAT GCT GCC ATC AAC AAC	288
Thr Gly Leu Leu Phe Gly Phe Thr Tyr Leu Tyr Ala Ala Ile Asn Asn	
85 90 95	
ACT TTC AAT CTC GAT TGG AAA CCC TAT GGC TGG TAT TGC TTG TTT GTA	336
Thr Phe Asn Leu Asp Trp Lys Pro Tyr Gly Trp Tyr Cys Leu Phe Val	
100 105 110	
ACC ATC AAC ACT ATC CCA GCG GCC ATT CTT TCT CAC TAT TCC GAT GCG	384
Thr Ile Asn Thr Ile Pro Ala Ala Ile Leu Ser His Tyr Ser Asp Ala	
115 120 125	
CTT GAT GAT CAC CGC CTC TTA GGA ATC ACT GAG GGC GAT TGG TGG GCT	432
Leu Asp Asp His Arg Leu Leu Gly Ile Thr Glu Gly Asp Trp Trp Ala	
130 135 140	
TTC ATT TGG CTT GCT TGG GGT GTT TTG TGG CTC ACT GGT TGG ATT GAA	480
Phe Ile Trp Leu Ala Trp Gly Val Leu Trp Leu Thr Gly Trp Ile Glu	
145 150 155 160	
TGC GCA CTT GGT AAG AGT CTA GGT AAA TTT GTT CCA TGG CTT GCC ATC	528
Cys Ala Leu Gly Lys Ser Leu Gly Lys Phe Val Pro Trp Leu Ala Ile	
165 170 175	

98

GTC GAG GGC GTG ATC ACC GCT TGG ATT CCT GCT TGG CTA CTC TTT ATC 576
 Val Glu Gly Val Ile Thr Ala Trp Ile Pro Ala Trp Leu Leu Phe Ile
 180 185 190

CAA CAC TGG TCT TGA
 591
 Gln His Trp Ser
 195

(2) INFORMATION FOR SEQ ID NO: 8:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 199 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:
 (A) ORGANISM : H. felis

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

Lys Gly Trp Met Leu Gly Leu Val Leu Leu Tyr Val Ala Val Val Leu
 1 5 10 15
 Ile Ser Asn Gly Val Ser Gly Leu Ala Asn Val Asp Ala Lys Ser Lys
 20 25 30
 Ala Ile Met Asn Tyr Phe Val Gly Gly Asp Ser Pro Leu Cys Val Met
 35 40 45
 Trp Ser Leu Ser Ser Tyr Ser Thr Phe His Pro Thr Pro Pro Ala Thr
 50 55 60
 Gly Pro Glu Asp Val Ala Gln Val Ser Gln His Leu Ile Asn Phe Tyr
 65 70 75 80
 Gly Pro Ala Thr Gly Leu Leu Phe Gly Phe Thr Tyr Leu Tyr Ala Ala
 85 90 95
 Ile Asn Asn Thr Phe Asn Leu Asp Trp Lys Pro Tyr Gly Trp Tyr Cys
 100 105 110
 Leu Phe Val Thr Ile Asn Thr Ile Pro Ala Ala Ile Leu Ser His Tyr
 115 120 125
 Ser Asp Ala Leu Asp Asp His Arg Leu Leu Gly Ile Thr Glu Gly Asp
 130 135 140
 Trp Trp Ala Phe Ile Trp Leu Ala Trp Gly Val Leu Trp Leu Thr Gly
 145 150 155 160
 Trp Ile Glu Cys Ala Leu Gly Lys Ser Leu Gly Lys Phe Val Pro Trp
 165 170 175

99

Leu Ala Ile Val Glu Gly Val Ile Thr Ala Trp Ile Pro Ala Trp Leu
180 185 190

Leu Phe Ile Gln His Trp Ser
195

CLAIMS

1. Immunogenic composition, capable of inducing antibodies against Helicobacter infection, characterised in that it comprises :

i) at least one sub-unit of a urease structural polypeptide from Helicobacter pylori, or a fragment thereof, said fragment being recognised by antibodies reacting with Helicobacter felis urease, and/or at least one sub-unit of a urease structural polypeptide from Helicobacter felis, or a fragment thereof, said fragment being recognised by antibodies reacting with Helicobacter pylori urease ;

ii) and/or, a Heat Shock protein (HSP), or chaperonin, from Helicobacter, or a fragment of said protein.

2. Immunogenic composition according to claim 1 capable of inducing protective antibodies.

3. Immunogenic composition according to claim 1 characterised in that it includes component (i), which comprises or consists of the Helicobacter felis urease structural polypeptide(s) encoded by the ure A and/or ure B genes of plasmid pILL205 (CNCM I-1355), a polypeptide exhibiting at least 90 % homology with the said polypeptide(s), or a fragment thereof having at least 6 amino-acids and being recognised by antibodies reacting with Helicobacter pylori urease.

4. Immunogenic composition according to claim 1, characterised in that it includes component ii) which is a HSP from Helicobacter pylori, or a fragment thereof.

5. Immunogenic composition according to any of preceding claims characterised in that the HSP is HSP A and/or HSP B encoded by the hsp A and/or hsp B genes respectively, of plasmid pILL689 (CNCM I-1356), or a

polypeptide exhibiting at least 75 % homology with the said HSP's, or a fragment of either or both of these proteins having at least 6 amino-acids.

6. Pharmaceutical composition for use as a vaccine in protecting against Helicobacter infection, particularly against Helicobacter pylori and Helicobacter felis, characterised in that it comprises the immunogenic composition of any of claims 1-5, in combination with physiologically acceptable excipient(s) and possibly adjuvants.

7. Proteinaceous material characterised in that it comprises at least one of the Helicobacter felis polypeptides encoded by the urease gene cluster of the plasmid pILL205 (CNCM I-1355), including the structural and accessory urease polypeptides, or a polypeptide having at least 90 % homology with said polypeptides, or a fragment thereof.

8. Proteinaceous material according to claim 7, characterised in that it consists of or comprises the gene product of ure A and/or ure B as illustrated in figure 3, or a fragment having at least 6 amino-acids, or a variant of these gene products having at least 90 % homology, said fragment and said variant being recognised by antibodies reacting with Helicobacter pylori urease.

9. Proteinaceous material according to claim 7 characterised in that it consists of or comprises the gene product of ure I, as illustrated in figure 9, or a fragment thereof having at least 6 amino-acids, or a variant of the gene product having at least 75 % homology, said fragment and said variant having the capacity to activate the ure A and ure B gene products in the presence of the remaining urease "accessory" gene products.

10. Nucleic acid sequence characterised in that it comprises :

- (i) at least one sequence coding for the proteinaceous material of any one of claims 6-9 ;
- or (ii) a sequence complementary to sequence (i) ;
- or (iii) a sequence capable of hybridising to sequences (i) or (ii) under stringent conditions ;
- iv) a fragment of any of sequences (i), (ii) or (iii) comprising at least 10 consecutive nucleotides.

11. Nucleic acid sequence according to claim 9 characterised in that it comprises the sequence of plasmid pILL205 (CNCM I-1355), for example the sequence of Figure 3, in particular that coding for the gene product of ure A and for ure B or the sequence of Figure 9 (Ure I), or a sequence capable of hybridising to these sequences under stringent conditions, or a sequence complementary to these sequences, or a fragment comprising at least 10 consecutive nucleotides of these sequences.

12. Expression vector characterised in that it contains a nucleic acid sequence according to claim 10 or 11.

13. Plasmid pILL205 (CNCM I-1355).

14. Oligonucleotide suitable for use as a primer in a nucleic acid amplification reaction, characterised in that it comprises from 10 to 100 consecutive nucleotides of the sequence of claim 10 or 11.

15. Nucleotide probe characterised in that it comprises a sequence according to any one of claims 9 or 10, with an appropriate labelling means.

16. Prokaryotic or eukaryotic host cell stably transformed by an expression vector according to claim 12 or 13.

17. Proteinaceous material characterised in that it comprises at least one of the Heat Shock Proteins (HSP), or chaperonins, of Helicobacter pylori, or a fragment thereof.

18. Proteinaceous material according to claim 17, characterised in that it comprises or consists of HSP A and/or HSP B, having the amino-acid sequence illustrated in Figure 6, or a polypeptide having at least 75 %, and preferably at least 80 % homology with said polypeptide, or a fragment thereof, comprising at least 6 amino-acids.

19. Proteinaceous material according to claim 18 characterised in that it comprises or consists of the HSP A C-terminal sequence :

G S C C H T G N H D H K H A K E H E A C C H D H K K H
or a fragment comprising at least 6 consecutive amino-acids of this sequence.

20. Nucleic acid sequence characterised in that it comprises :

i) a sequence coding for the proteinaceous material of any one of claims 17 to 19 or of any one of the proteinaceous materials of claims 7 to 9 ;
or ii) a sequence complementary to sequence (i) ;
or iii) a sequence capable of hybridizing to sequence (i) or (ii) under stringent conditions ;
or iv) a fragment of any of sequences (i), (ii) or (iii) comprising at least 10 nucleotides.

21. Nucleic acid sequence according to claim 20 characterised in that it comprises all or part of the sequence of plasmid pILL689 (CNCM I-1356), for example the sequence of figure 6, in particular that coding for HSP A and/or HSP B, or a sequence complementary to this sequence, or a sequence capable of hybridizing to this sequence under stringent conditions, or a fragment thereof.

22. Expression vector characterised in that it contains a nucleic acid sequence according to claim 20 or 21.

23. Plasmid pILL689 (CNCM I-1356).

24. Oligonucleotide suitable for use as a primer in a nucleic acid amplification reaction, characterised in that it comprises from 10 to 100 consecutive nucleotides of the sequence of claim 20 or 21.

25. Nucleotide probe, characterised in that it comprises a sequence according to any one of claims 20 or 21 with an appropriate labelling means.

26. Microorganism, stably transformed by an expression vector according to claim 22 or 23.

27. Monoclonal or polyclonal antibodies or fragments thereof, to the proteinaceous material of any one of claims 8 to 10, characterised in that they are either specific for the Helicobacter felis material, or alternatively, cross-react with the gene products of the urease gene cluster of Helicobacter pylori.

28. Monoclonal or polyclonal antibodies according to claim 27 characterised in that they recognise both the Helicobacter felis ure A and/or ure B gene product, and the Helicobacter pylori ure A and/or ure B gene product.

29. Monoclonal or polyclonal antibodies or fragments thereof, to the proteinaceous material of claims 17 or 18, characterised in that they are either specific for the Helicobacter pylori material or, alternatively, cross-react with GroEL-like proteins or GroES-like proteins from bacteria other than Helicobacter.

30. Monoclonal or polyclonal antibodies according to claim 29 characterised in that they recognise specifically the HSP A C-terminal sequence.

31. Use of the immunogenic composition of claim 1 for the preparation of a vaccine suitable for use in man and animals against Helicobacter infection, particularly against Helicobacter pylori and Helicobacter felis.

32. Use of the antibodies of claims 27 to 30 in a therapeutic composition for treating infection by Helicobacter, in particular Helicobacter pylori, Helicobacter heilmannii and Helicobacter felis in man or animals.

33. Method for the production of a pharmaceutical composition according to claim 6, characterised by culturing a transformed micro-organism according to claim 16, and optionally, also a micro-organism according to claim 26, collecting and purifying the Helicobacter urease polypeptide material and where applicable, also the HSP material, and combining these materials with suitable excipients, adjuvants and, optionally, other additives.

34. Use of nucleotide sequences of any claim 15 or 25 for the in vitro detection in a biological sample, of an infection by Helicobacter, optionally following a gene amplification reaction.

35. Kit for the in vitro detection of Helicobacter infection, characterised in that it comprises :

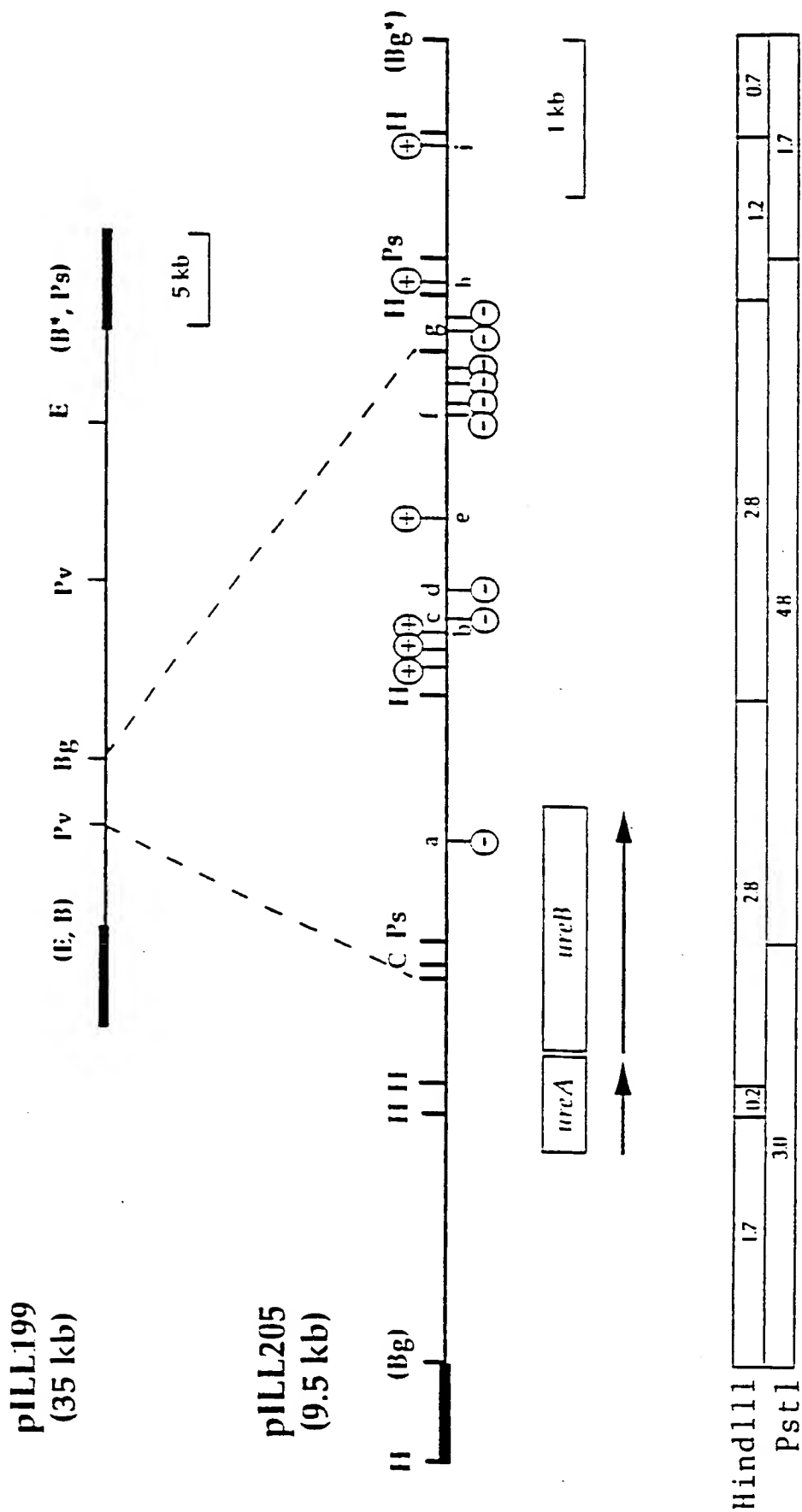
- a nucleotide probe according to claim 15 or 25 ;
- an appropriate medium for carrying out a hybridisation reaction between the nucleic acid of Helicobacter and the probe ;

- reagents for the detection of any hybrids formed.

36. Proteinaceous material characterised in that it comprises a fusion or mixed protein including at least one sub-unit of a urease structural polypeptide from Helicobacter pylori or fragment thereof, or from Helicobacter felis or fragment thereof as defined in claims 1 to 3, 5, 7 to 9, and or a heat shock proteins (HSP) from Helicobacter or fragment thereof, as defined in claims 17 to 20.

37. Purified antibodies or serum obtained by immunisation of an animal with the immunogenic composition according to claims 1 to 5, or with the proteinaceous material or fragment of claims 7 to 9 or 17 to 19, or with the fusion or mixed protein of claims 36.

38. Kit comprising at least the purified antibodies or serum according to claim 37, and optionally, appropriate media or excipients for administration of the antibodies, or labelling or detection means for the antibodies.



- FIGURE 1 -

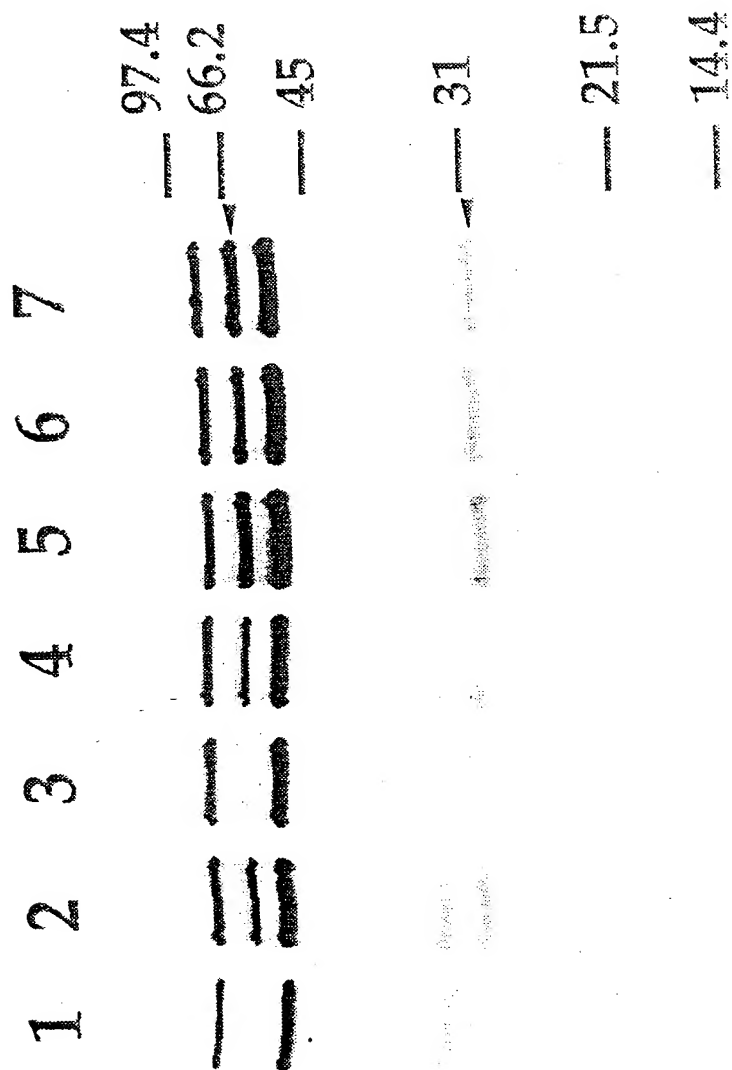


FIGURE 2 A

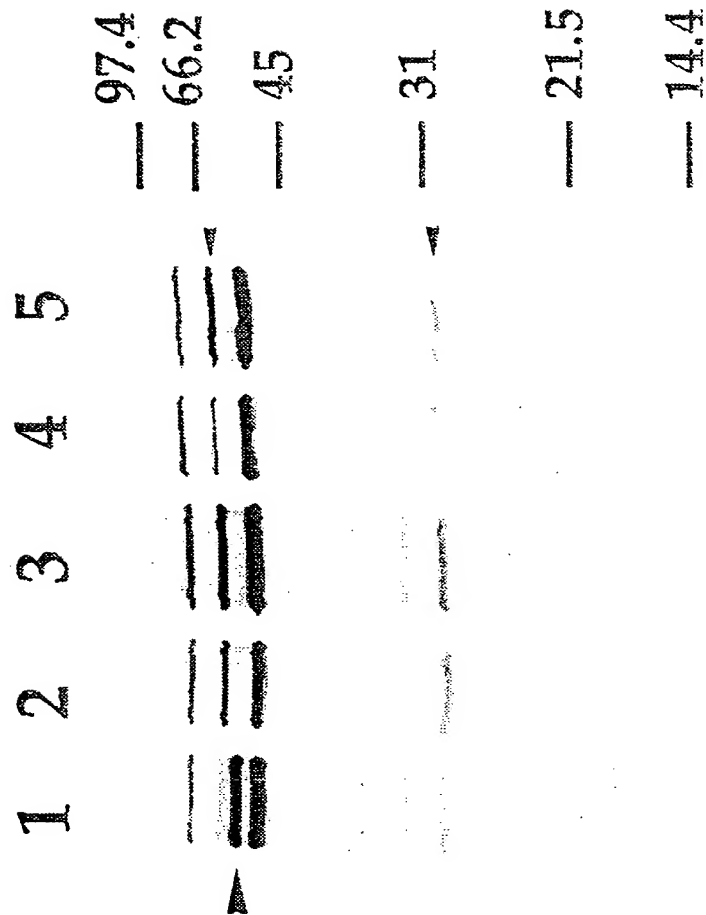


FIGURE 2 B

1 31 SD
 TGA TAG CTT GGC TAC CAA TAG AAA TTC AAT AAG GAG TTT AGG ATG AAA CTA ACG CCT AAA
 ureA Met lys leu thr pro lys
 61/7 91/17
 GAA CTA GAC AAG TTA ATG CTC CAT TAT GCG GGC AGA TTG GCA GAA CGC TTG GCG CGT
 glu leu asp lys leu met leu his tyr ala gly arg leu ala glu arg leu ala arg
 121/27 151/37
 GGT GTG AAA CTC AAT TAC ACC GAA GCG GTC ATT AGC GGG CGT GTG ATG GAA AAG
 gly val lys leu asn tyr thr glu ala val ala leu ile ser gly arg val met glu lys
 181/47 211/57
 GCG CGT GAT GGT AAT AAA AGC GTG GCG GAT TTG ATG CAA GAA GGC AGG ACT TGG CTT AAA^{4/56}
 ala arg asp gly asn lys ser val ala asp leu met gln glu gly arg thr trp leu lys
 241/67 271/77
 AAA GAA AAT GTG ATG GAC GGC GTA GCA AGC ATG ATT CAT GAA GTG GGG ATT GAA GCT AAC
 lys glu asn val met asp gly val ala ser met ile his glu val gly ile glu ala asn
 301/87 331/97
 TTC CCC GAT GGA ACC AAG CTT GTA ACT ATC CAC ACT CCG GTA GAG GAT AAT GGC AAA TTA
 phe pro asp gly thr lys leu val thr ile his thr pro val glu asp asn gly lys leu
 361/107 391/117
 GCC CCC GGC GAG GTC TTC TTA AAA AAT GAG GAC ATT ACT ATT AAC GCC GGC AAA GAA GCC
 ala pro gly glu val phe leu lys asn glu asp ile thr ile asn ala gly lys glu ala

- FIGURE 3 (1) -

5/56

421/127 451/137
 ATT AGC TTG AAA GTG AAA AAT AAA GGC GAT CGT CCT GTG CAG GTG GGA TCA CAT TTC CAC
 ile ser leu lys val lys asn lys gly asp arg pro val gln val gly ser his phe his
 481/147 511/157
 TTC TTC GAA GTG AAT AAG CTC TTG GAC TTC GAT CGC GCA AAA AGC TTT TGC AAA CGC CTA
 phe phe glu val asn lys leu leu asp phe asp arg ala lys ser phe cys lys arg leu
 541/167 571/177
 GAC ATT GCA TCT GGA ACA GCG GTG CGC TTT GAA CCC GGG GAG GAA AAA AGT GTG GAA CTC
 asp ile ala ser gly thr ala val arg phe glu pro gly glu glu lys ser val glu leu
 601/187 631/197
 ATT GAC ATC GGC GGC AAT AAG CGC ATC TAT GGC TTT AAT TCT TTG GTG GAT CGC CAA GCC
 ile asp ile gly gly asn lys arg ile tyr gly phe asn ser leu val asp arg gln ala
 661/207 691/217
 GAT GCC GAT GGT AAA AAA CTC GGC TTA AAA CGC GCT AAA GAA AAA GGT TTT GGG TCT GTA
 asp ala asp gly lys lys leu gly leu lys arg ala lys glu lys gly phe gly ser val
 721/227 751 SD
 AAC TGC GGT TGT GAA GCG ACT AAA GAT AAA CAA TAA GGA AAA ACC ATG AAA AAG ATT TCA
 asn cys gly cys glu ala thr lys asp lys gln OCH ureB Met lys lys ile ser
 781/6 811/16
 CGA AAA GAA TAT GTT TCT ATG TAT GGT CCC ACT ACC GGG GAT CGT GTT AGA CTC GGC GAC
 arg lys glu tyr val ser met tyr gly pro thr thr gly asp arg val arg leu gly asp

- FIGURE 3 (ii) -

841/26
ACT GAT TTG ATC TTA GAA GTG GAG CAT GAT TGC ACC ACT TAT GGT GAA GAG ATC AAA TTT
thr asp leu ile leu glu val glu his asp cys thr thr tyr gly glu ile lys phe
901/46
GGG GGC GGT AAA ACT ATC CGT GAT GGG ATG AGT CAA ACC AAT AGC CCT AGC TCT TAT GAA
gly gly gly lys thr ile arg asp gly met ser gln thr asn ser pro ser tyr glu
961/66
TTA GAT TTG GTG CTC ACT AAC GCC CTC ATT GTG GAC TAT ACG GGC ATT TAC AAA GCC GAC
leu asp leu val leu thr asn ala leu ile val asp tyr thr gly ile tyr lys ala asp
1021/86
ATT GGG ATT AAA GAC GGC AAG ATT GCA GGC AAG GCA GGC AAT AAG GAC ATG CAA
ile gly ile lys asp gly lys ile ala gly ile gly lys ala gly asn lys asp met gln
1081/106
GAT GGC GTA GAT AAT AAT CTT TGC GTA GGT CCT GCT ACA GAG GCT TTG GCA GCT GAG GGC
asp gly val asp asn asn leu cys val gly pro ala thr glu ala leu ala ala glu gly
1141/126
TTG ATT GTA ACC GCT GGT GGC ATC GAT ACG CAT ATT CAC TTT ATC TCT CCC CAA CAA ATC
leu ile val thr ala gly gly ile asp thr his ile his phe ile ser pro gln gln ile
1201/146
CCT ACT GCT TTT GCC AGC GGG GTT ACA ACC ATG ATT GGA GGC ACA GGA CCT GCG GAT
pro thr ala phe ala ser gly val thr thr met ile gly gly thr gly pro ala asp

7/56

1261/166
 GGC ACG AAT GCG ACC ACC ATC ACT CCC GGA CGC GCT AAT CTA AAA AGT ATG TTG CGT GCA
 gly thr asn ala thr thr ile thr pro gly arg ala asn leu lys ser met leu arg ala
 1321/186
 1291/176
 GCC GAA GAA TAC GCC ATG AAT CTA GGC TTT TTG GCT AAG GGG AAT GTG TCT TAC GAA CCC
 ala glu glu tyr ala met asn leu gly phe leu ala lys gly asn val ser tyr glu pro
 1381/206
 1411/216
 TCT TTA CGC GAT CAG ATT GAA GCA GGC GCG ATT GGT TTT AAA ATC CAC GAA GAC TGG GGA
 ser leu arg asp gln ile glu ala gly ala ile gly phe lys ile his glu asp trp gly
 1441/226
 1471/236
 AGC ACA CCT GCA GCT ATT CAC CAC TGC CTC AAT GTC GCC GAT GAA TAC GAT GTG CAA GTG
 ser thr pro ala ala ile his his cys leu asn val ala asp glu tyr asp val gln val
 1501/246
 1531/256
 GCT ATC CAC ACC GAT ACC CTT AAC GAG GCG GGC TGT GTA GAA GAC ACC CTA GAG GCG ATT
 ala ile his thr asp thr leu asn glu ala gly cys val glu asp thr leu glu ala ile
 1561/266
 1591/276
 GCC GGC CGC ACC ATC CAT ACC TTC CAC ACT GAA GGC GCT GGG GGT GGA CAC GCT CCA GAT
 ala gly arg thr ile his thr phe his thr glu gly ala gly gly his ala pro asp
 1621/286
 1651/296
 GTT ATC AAA ATG GCA GGC GAA TTT AAC ATT CTA CCC GCC TCT ACT AAC CCG ACC ATT CCT
 val ile lys met ala gly glu phe asn ile leu pro ala ser thr asn pro thr ile pro
 1681/306
 1711/316
 TTC ACC AAA AAC ACT GAA GCC GAG CAC ATG GAC ATG TTA ATG GTG TGC CAC CAC TTG GAT
 phe thr lys asn thr glu ala glu his met asp met leu met val cys his his leu asp

- FIGURE 3 (iv)

8/56

1741/326
 AAA AGT ATC AAG GAA GAT GTG CAG TTT GCC GAT TCG AGG ATT CGC CCC CAA ACT ATC GCG
 lys ser ile lys glu asp val gln phe ala asp ser arg ile arg pro gln thr ile ala
 1801/346
 GCT GAA GAC CAA CTC CAT GAC ATG GGG ATC TTT TCT ATC ACC AGC TCC GAC TCT CAG GCT
 ala glu asp gln leu his asp met gly ile phe ser ile thr ser ser asp ser gln ala
 1861/366
 ATG GGA CGC GTA GGC GAG GTG ATC ACA CGC ACT TGG CAG ACA GCA GAC AAA AAC AAA AAA
 met gly arg val gly glu val ile thr arg thr trp gln thr ala asp lys asn lys lys
 1921/386
 GAG TTT GGG CGC TTG AAA GAG GAA AAA GGC GAT AAC GAC AAC TTC CGC ATC AAA CGC TAC
 glu phe gly arg leu lys glu glu lys lys gly asp asn asp asn phe arg ile lys arg tyr
 1981/406
 ATC TCT AAA TAC ACC ATC AAC CCC GGG ATC GCG CAT GGG ATT TCT GAC TAT GTG GGC TCT
 ile ser lys tyr thr ile asn pro gly ile ala his gly ile ser asp tyr val gly ser
 2041/426
 GTG GAA GTG GGC AAA TAC GCC GAC CTC GTG CTT TGG AGT CCG GCT TTC TTT GGC ATT AAG
 val glu val gly lys tyr ala asp leu val leu trp ser pro ala phe phe gly ile lys
 2101/446
 CCC AAT ATG ATT ATT AAG GGC GGA TTT ATT GCG CTC TCT CAA ATG GGC GAT GCC AAT GCG
 pro asn met ile ile lys gly gly phe ile ala leu ser gln met gly asp ala asn ala
 2161/466
 TCT ATT CCC ACC CCT CAG CCC GTC TAT TAC CGT GAA ATG TTT GGA CAC CAT GGC AAA AAC
 ser ile pro thr pro gln pro val tyr tyr arg glu met phe gly his his gly lys asn

- FIGURE 3 (v) -

2221/486 2251/496
 AAA TTC GAC ACC AAT ATC ACT TTC GTG TCC CAA GCG GCT TAC AAG GCA GGG ATC AAA GAA
 lys phe asp thr asn ile thr phe val ser gln ala ala tyr lys ala gly ile lys glu
 2281/506 2311/516
 GAA CTA GGG CTA GAT CGC GCG GCA CCG CCA GTG AAA AAC TGT CGC AAT ATC ACT AAA AAG
 glu leu gly leu asp arg ala ala pro pro val lys asn cys arg asn ile thr lys lys
 2341/526 2371/536
 GAC CTC AAA TTC AAC GAT GTG ACC GCA CAT ATT GAT GTC AAC CCT GAA ACC TAT AAG GTG
 asp leu lys phe asn asp val thr ala his ile asp val asn pro glu thr tyr lys val
 2401/546 2431/556
 AAA GTG GAT GGC AAA GAG GTA ACC TCT AAA GCA GCA GAT GAA TTG AGC CTA GCG CAA CTT
 lys val asp gly lys glu val thr ser lys ala ala asp glu leu ser leu ala gln leu
 2461/566 2491
 TAT AAT TTG TTC TAG GAG GCT AAG GAG GGG GAT AGA GGG GGT TAA TTT AGA GGG GAG TCA
 tyr asn leu phe AMB
 2521 2551
 TTG ATT TAC CTT TGC TAG TTT ATA ATG GAT TTA AGA GAG GTT TTT CGT GTT TTA TAC

 2581 2611
 CGC GTT GAA ACC CTC AAA TCT TTA CCA AAA GGA TGG TAA

urea

H. f.
H. p.
P. m.
J. b.

```

      . . . .
MKLTPKELDKMLHIYAGRLAEERLARGVKLNYTEAVALLISGRVME
*****E**KKRKEK*I***V*****AHI**
**E**R*K**L*FT**LV**RR**K*L***P*R*****CAI**
**S*R*VE**G**N**Y**QKR*****R***T*****ASQI**
= = = = = = = = = = = = = = = = = = = = = =

```

```

      . . . . . . . . . .
KARDGNKSVADLMQEGRTWLKKNVMDGVASMIHEVGIEANFPDG 89
E**A*K*TA*E*****L**PDD*****M*** 89
G**E*-T**Q**S***V*TA*Q**E**PE**KD*QV*CT*** 89
Y***E*T**Q**CL*QHL*GRRQ*LPA*PHLLNA*QV**TE*** 90
= = = = = = = = = = = = = = = = = = = = = =

```

- FIGURE 4 (i) -

12/56

H. f. DEDRAKSFCKRLDIASGTA VRFEPGEEKSV-ELIDIGGNKRIY
H. P. ***E*T*G*****-*****R**F
P. m. R*A*KETLGF**N*PA*M*****QSRT*D**VAFA*KRE**
J. b. T***R*AYGM**N**AG*****DC***-T*VS*E**KV*R
=====

.
GFNSLVDRQADADGKKLGLKRAKEKF-GSVNCGCEAT---KDKQ
A**NES**IA**R**AKSDDNYVKTI-*E
-----**KVMGGLESE--K*
*GAIA*GPVNETNLEAMHIAVRSR*-HEEEKDAPEGFT*EDPNC SF-270

- FIGURE 4 (iii) -

ureB

H.f.
H.p.
P. m.
J.b.

```

      .      . .      .      .      .      .
MKKISRKEYVSMYGP'TTGDRVRLGDTDLILEVEHDC
*****
**T**Q**A**D**F*****L**A**F**F**I**K**F
NTF**H*****ANK*****KI*****N**L**I**K**Y
= = = = =
=====
= = = = =

```

```

      .      .      .      .      .      .
TTYGEEIKFGGGKTIRDGMSQTNSSPYEL-DLVLTNALIVDYTGI 81
*I**A**I*****L**E*****S**N**K**E**--**I**I***** 81
*****V*****V*****G**SQVV**NECV--*VL**I*****I**L**W** 81
AL**D**CV*****V*****G**SCGHPPI**SI**T**I*****V**I***** 352
=====
= = = = =

```

```

      .      .      .      .      .      .      .      .      .      .
YKADIGIKDKIAGIGKAGNKDMQDGVDDNNLCVGPATEALAAEGL
*****G*****K*****S*****G***
V*****R*****P*VQPN**IVI--**G**VV**G**K
I*****L**S*****P*IMN**FSNMI I**AN**VI *G***
===== = === = = = = = = = =

```

H.f.
H.P.
P. m.
J.b.

```

      .      .      .      .      .      .      .      .      .      .
IVTAGGIDTHIHFISPOQIPTAFASGVTTMIGGGTGPADGTNATT 171
*****
*****C**AQEGLV***FI*****VA***** 169
*****C**Y**C**LVYEAI**I**LV*****A**R** 442
===== = === = = = = = = = =

```

H.f.
 ITPGRANLKSMLRAAEYAMNLGFLAKGNVSYEPSLRDQIEAGAI
H.p. ***R***W***S***A***A***A***A***
p. m. V***IW*MYR**E*VD*LPI*V*LFG**CV*QPEAI*E**T***
J.b. C**SPTQMRL**QSTDDLPL*F**TG**SS*KPDE*HEI*K***M
 == = = = ==

.
 GFKIHEDWGSTPAAIHHCLNVADEYDVQVAIHTDTLNEAGCVEDT 261
 *****T**S**N*A*D***K***** 261
 *L*****A**M*****N*****M*****S*****G*FY*E* 259
 *L*L*****DN**TI*EHH*I*IN*****F**HS 532
 = = ===== = = = = = = = =

- FIGURE 4 (vi) -

H.f.	NDVTAHIDVNPETYKVKVDGKEVTSKAADELSLAQLYNLF	569
H.p.	**T***E*****H*F*****P*NKV*****F*SI*	569
P. m.	*NYVP**ELD*Q**I**A**VPLVCEP*T**PM**R**F**	569
J.b.	**ALPE*T*D**S*T**A**LLCVSE*TTVP*SRN*F**	840
	=	=
	ureA : 74 % Identity	ureB : 88 % Identity
	ureA : 46 % Identity	ureB : 62 % Identity
	ureA : 47 % Identity	ureB : 59 % Identity

FIGURE 4 (x)

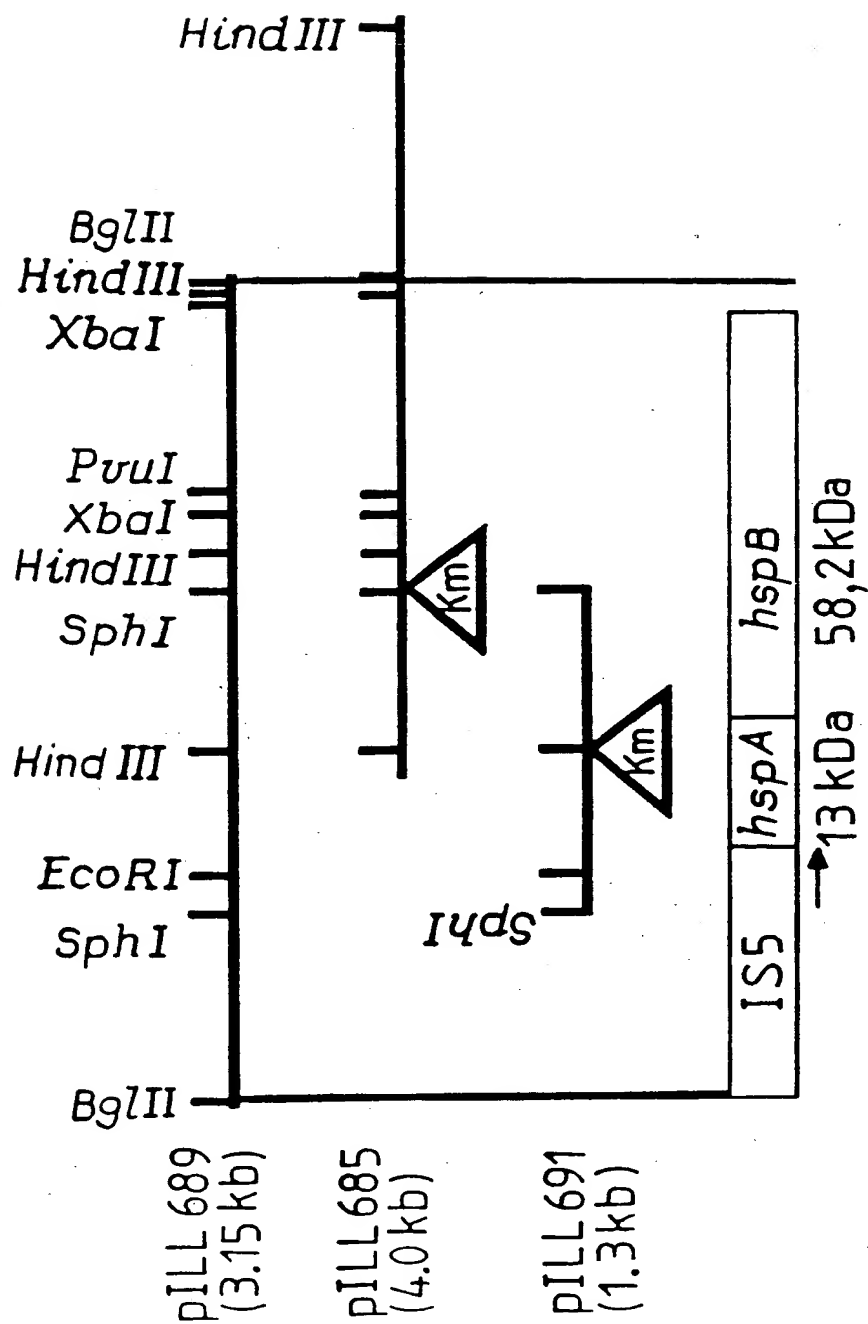


FIGURE 5

21/56

```

1      ACA AAC ATG ATC TCA TAT CAG GGA CTT GTT CGC ACC TTC CCT AAA AAT GCG CTA TAG TTG
31
61      TGT CGC TTA AGA ATA CTA AGC GCT AAA TTT CTA TTT TAT TTA TCA AAA CTT AGG AGA ACT
91
121     GAA ATG AAG TTT CAA CCA TTA GGA GAA AGG GTC TTA GTA GAA AGA CTT GAA GAA GAG AAC
      met lys phe gln pro leu pro leu gly glu arg val leu val glu arg leu glu glu asn
151/10
181/21  AAA ACC AGT TCA GGC ATC ATC ATC CCT GAT AAC GCT AAA GAA AAG CCT TTA ATG GGC GTA
      lys thr ser ser gly ile ile ile pro asp asn ala lys glu lys pro leu met gly val
211/31
241/41  GTC AAA GCG GTT AGC CAT AAA ATC AGT GAG GGT TGC AAA TGC GTT AAA GAA GGC GAT GTG
      val lys ala val ser his lys ile ser glu gly cys lys cys val lys glu gly asp val
271/51
301/51  ATC GCT TTT GGC AAA TAC AAA GGC GCA GAA ATC GGT TTA GAT GGC GTT GAA TAC ATG GTG
      ile ala phe gly lys tyr lys gly ala glu ile val leu asp gly val glu tyr met val
331/71
361/71  CTA GAA CTA GAA GAC ATT CTA GGT ATT GTG GGC TCA GGC TCT TGC TGT CAT ACA GGT AAT
      leu glu leu glu asp ile leu gly ile val gly ser gly ser cys cys his thr gly asn
391/91
421/91  CAT GAT CAT AAA CAT GCT AAA GAG CAT GAA GCT TGC TGT CAT GAT CAC AAA AAA CAC TAA
      his asp his lys his ala lys glu his glu ala cys cys his asp his lys lys his OCH
451/111
481     AAA ACA TTA TTA TTA AGG ATA CAA AAT GGC AAA AGA
511

```

- FIGURE 6 (1) -

22/56

479 AAA AAA CAT TAT TAT TAA GGA TAC AAA ATG GCA AAA GAA ATC AAA TTT TCA GAT AGC GCA
 509/2 met ala lys glu ile lys phe ser asp ser ala
 539/12 AGA AAC CTT TTA TTT GAA GGC GTA AGA CAA CTC CAT GAC GCT GTC AAA GTA ACC ATG GGG
 arg asn leu leu phe glu gly val arg gln leu his asp ala val lys val thr met gly
 569/22
 599/32 CCA AGA GGC AGG AAC GTG TTG ATC CAA AAA AGC TAT GGC GCT CCA AGC ATC ACC AAA GAC
 pro arg gly arg asn val leu ile gln lys ser tyr gly ala pro ser ile thr lys asp
 629/42
 659/52 GGC GTG AGC GTG GCT AAA GAG ATT GAA TTA AGT TGC CCC GTG GCT AAC ATG GGC GCT CAG
 gly val ser val ala lys glu ile glu leu ser cys pro val ala asn met gly ala gln
 689/62
 719/72 CTC GTT AAA GAA GAT GCG AGC AAA ACC GCT GAT GCC GCC GGC GAT GGC ACC ACA GCG
 leu val lys glu asp ala ser lys thr ala asp ala ala gly asp gly thr thr ala
 749/82
 779/92 ACC GTG CTG GCT TAT AGC ATT TTT AAA GAG GGC TTG AGG AAT ATC ACG GCT GGG GCT AAC
 thr val leu ala tyr ser ile phe lys glu gly leu arg asn ile thr ala gly ala asn
 809/102
 839/112 CCT ATT GAA GTG AAA CGA GGC ATG GAT AAA GCG CCT GAA GCG ATC ATT AAT GAG CTT AAA
 pro ile glu val lys arg gly met asp lys ala pro glu ala ile ile asn glu leu lys
 869/122
 899/132 AAA GCG AGC AAA AAA GTG GGC GGT AAA GAA GAA ATC ACC CAA GTA GCG ACC ATT TCT GCA
 lys ala ser lys lys val gly gly lys glu glu ile thr gln val ala thr ile ser ala
 929/142

- FIGURE 6 (ii) -

23/56

959/152 AAC TCC GAT CAC AAT ATC GGG AAA CTC ATC GCT GAC GCT ATG GAA AAA GTG GGT AAA GAC
 asn ser asp his asn ile ile gly lys lys leu ile ala asp ala met glu lys val gly lys asp
 989/162
 1019/172 GGC GTG ATC ACC GTT GAA GAA GCT AAG GGC ATT GAA GAT GAA TTA GAT GTC GTA GAA GGC
 gly val ile thr val glu glu ala lys gly ile glu asp glu leu asp val val glu gly
 1049/182
 1079/192 ATG CAA TTT GAT AGA GGC TAC CTC TCC CCT TAC TTT GTA ACC AAC GCT GAG AAA ATG ACC
 met gln phe asp arg gly tyr leu ser pro tyr phe val thr asn ala glu lys met thr
 1109/202
 1139/212 GCT CAA TTG GAT AAC GCT TAC ATC CTT TTA ACG GAT AAA AAA ATC TCT AGC ATG AAA GAC
 ala gln leu asp asn ala tyr ile leu leu thr asp lys lys ile ser ser met lys asp
 1169/222
 1199/232 ATT CTC CCG CTA GAA AAA ACC ATG AAA GAG GGC AAA CCG CTT TTA ATC ATC GCT GAA
 ile leu pro leu leu leu lys thr met lys gly gly lys pro leu leu ile ile ala glu
 1229/242
 1259/252 GAC ATT GAG GGC GAA GCT TTA ACG ACT CTA GTG GTG AAT AAA TTA AGA GGC GTG TTG AAT
 asp ile glu gly glu ala leu thr thr leu val val asn lys leu arg gly val leu asn
 1289/262
 1319/272 ATC GCA GCG GTT AAA GCT CCA GGC TTT GGG GAC AGG AGA AAA GAA ATG CTC AAA GAC ATC
 ile ala ala val lys ala pro gly phe gly asp arg arg lys glu met leu lys asp ile
 1349/282

24/56

1379/292	1409/302
GCT GTT TTA ACC GGC GGT CAA GTC ATT AGC GAA GAA TTG GGC TTG AGT CTA GAA AAC GCT	
ala val leu thr gln val ile ser glu glu leu gly leu ser leu glu asn ala	
1439/312	1469/322
GAA GTG GAG TTT TTA GGC AAA GCG AAG ATT GTG ATT GAC AAA GAC AAC ACC ACG ATC GTA	
glu val glu phe leu gly lys ala lys ile val ile asp lys asp asn thr thr ile val	
1499/332	1529/342
GAT GGC AAA GGC CAT AGC CAT GAC GTC AAA GAC AGA GTC GCG CAA ATC AAA ACC CAA ATT	
asp gly lys gly his ser his asp val lys asp arg val ala gln ile lys thr gln ile	
1559/352	1589/362
GCA AGC ACC ACA AGC GAT TAC GAC AAA GAA AAA TTG CAA GAA AGA TTG GCC AAA CTC TCT	
ala ser thr thr ser asp tyr asp lys glu lys leu gln glu arg leu ala lys leu ser	
1619/372	1649/382
GGC GGT GTG GCT GTG ATT AAA GTG GGC GCT GCT GAA GTG GAA ATG AAA GAG AAA AAA	
gly gly val ala val ile lys val gly ala ala ser glu val glu met lys glu lys lys	
1679/392	1709/402
GAC CGG GTG GAT GAC GCG TTG AGC GCG ACT AAA GCG GCG GTT GAA GAA GGC ATT GTG ATT	
asp arg val asp asp ala leu ser ala thr lys ala ala val glu glu gly ile val ile	
1739/412	1769/422
GGG GGC GGT GCG GCC CTC ATT CGC GCG GCC CAA AAA GTG CAT TTG AAT TTA CAC GAT GAT	
gly gly gly ala ala leu ile arg ala ala gln lys val his leu asn leu his asp asp	

- FIGURE 6 (iv) -

25/56

1799/432 1829/442
 GAA AAA GTG GGC TAT GAA ATC ATC ATG CGC GCC ATT AAA GCC CCA TTA GCT CAA ATC GCT
 glu lys val gly tyr glu ile ile met arg ala ile lys ala pro leu ala gln ile ala

 1859/452 1889/462
 ATC AAT GCC GGT TAT GAT GGC GGT GTG GTC GTG AAT GAA GTA GAA AAA CAC GAA GGG CAT
 ile asn ala gly tyr asp gly gly val val val asn glu val glu lys his glu gly his

 1919/472 1949/482
 TTT GGT TTT AAC GCT AGC AAT GGC AAG TAT GTG GAC ATG TTT AAA GAA GGC ATT ATT GAC
 phe gly phe asn ala ser asn gly lys tyr val asp met phe lys glu gly ile ile asp

 1979/492 2009/502
 CCC TTA AAA GTA GAA AGG ATC GCT TTA CAA AAT GCG GTT TCG GTT TCA AGC CTG CTT TTA
 pro leu lys val glu arg ile ala leu gln asn ala val ser val ser leu leu leu

 2039/512 2069/522
 ACC ACA GAA GCC ACC GTG CAT GAA ATC AAA GAA GCG GCC CCA GCA ATG CCT GAT
 thr thr glu ala thr val his glu ile lys glu glu lys ala ala pro ala met pro asp

 2099/532 2129/542
 ATG GGT GGC ATG GGC GGA ATG GGA GGC ATG GGC ATG TAA GCC CCC TTG CTT TTT
 met gly gly met gly gly met gly gly met met OCH

 2159 2189
 GGT ATC ATC TGC TTT TAA AAT CCA TCT TCT AGA ATC CCC CCT TCT AAA ATC CCT TTT TTG

 2219 2249
 GGG GGT GCT TTT GGT TTG ATA AAA CCG CTC GCT TTT AAA AAC GCG CAA CAA AAA ACT CTG

 2279
 TTA AGC

- FIGURE 6 (v) -

26/56

MAKEIKFSDSARNLLFEGVRQLHDAVKVTMGPRGRNVLIQKSYG
 LR*G*D**LQMLA**NA**AQ***VLE***
 MA**DV**GND**VKMLR**NV**A***L**K***VLD**F*
 MA**N**YNED**KKIHK**KT*AE***L**K**H*V*D**F*
 T*AYDEE**RG*ER*LNS*AL**K***VLE*KW*
 Y**DV**-**GAD**ALMLQ**DL*A***A***K**T*I*EQ*W*

APSITKDGVSVAKEIELSCPVANMGAQLVKEDASKTADAAGDG
 TV*FHRFM***M**V***S*T***
 T*R***EDKFE***M**V**AN***
 S*QV***T***EDKHE***M**V***K***
 TN***I***ED*YEKI**E***V*K*D*V***
 S*KV***T***S*D*KDKYK*I**K**QDV*NN*NEE***

- FIGURE 7 A (1) -

27/56

TTTATVLAYSIFKEGLRNITAGANPIEVKRGMDKAPEAIINELKK
 *****LV**HKAVA**M**MDL**I**VL*VTKK*QA
 *****QA*IT**KAVA**M**MDL**I**VT*AVE***A
 *****EA*YS*****V*****MLD**I**VKVVVD*I**
 *****QALV*****VA*****LGL**IE**VDKVTET*L*
 *****R**A**FEK*SK*****VEIR**V*L*VD*V*A***

ASKKVGGKEEITQVATISANSDHNIGKLIADAMEKVGKDGVIT
 M**PCKDSKA*A**G*****EA**AI**E*****E****
 L*VPCSDSKA*A**G*****ETV*****E**D***E****
 I**P*QIIHK**A*****N**AE**N**E*****N*S**
 DA*E*ET**Q*AA*T*A**G*QS**D**E**D**NE****
 Q**P**TTP**A*****G*KE**NI*SD**K**RK***

- FIGURE 7 A (ii) -

28/56

VEEAKGIEDELDVVVEGMQFDRGYLSPYFVTNAEKMTAQLDNAYIL
 DGN*L*NY**I**IN*QON*SCE*EHPF**
 DGT*LQI**INKP*TGAVE*ESPF**
 ****F*TV**N**S**P*QECV*EE*LV*
 SNTFGLQ*ELTR**K**I**G**D**RQE*V*EEP***
 *KDG*TLN**EII**K**I**INTSKGQKCEFQD**V*

LTDKKISSMKDILPILLEKTMKEGKPLLIAEDIEGEALTTLVV
 *V**V**IREM*SV**GVA*S*R**I**A***
 *A**NIREM**V**AVA*A**V**A**A**
 IY**GI**F**V*QQVAES*R**A**A**
 *VSS*V*TV**L**VIQA**S**V**S**
 *SE***IQS*V*A**IANLVLNR*KVGLQVVAVK*PGF**L

- FIGURE 7 A (iii) -

29/56

NKLRGVI, NIAAVKAPGFGDRRKEMI, KDIAVL, TGGQVISEELGLSL,
 *NM*IVKVC*****A**Q**I**K*****I*K**
 *TI*IVKV*****A**Q**T*****T*****I*ME*
 *R*AGFRVC*****A**E**I*****L*****MK*
 *I*TFKSV*****A**Q**M**I**A*****V**T*
 *R*KVG*QVV*V*****N**NQ**K**M**IA**A*FG**GLTLN

ENAEVEF-LGKAKI-VIDKDNTTIVDGKGHSHDVKDRVAQIKT
 *G*TL*D-*S**RI*VT*E*****I**E*KATEINA*I**RA
 *K*TL*D-*Q**RV**N**T***I**V*EEAIIQG*****RQ
 *TTLAM-*K**KVIVS*ED*****E*L*SKE*IES*CES**K
 *TDLSL-*R**RKV*MT**E*****E*A*D'DAIAG*****R*
 LEDVQPHD**VGEVIVT**DAMLK*K*DKAQIEK*IQE*IE

- FIGURE 7 A (iv) -

30/56

QIASTTSYDKEKLQERLAKLSGGVAVIKVGAASEVEMKEKCD
 *MEE*****V**A*****T*****A
 EEA***V**A*****T*****A
 EDS***R*****T*I*****
 E*ENSD*****A*****T**L**R**H
 *LDV***E*EK**N*****SD**L***GT*D**VN***

RVDDALSATKAAVEEGIVIGGGAALIRAAQKVH---LN-LHDDEK
 EH**R*****A***V***QKALDS--*KGDN**QN
 EH**R*****V**A***V***S*LAD--*RGQNE*QN
 QHA*L**LP***T**V*CIP'TLEAFIPILTNE**Q
 *IE**VRNA*****A***VT*LQ**PALDK--*K-*TG**A
 TN**R*****L**C*L*CIPALDS--*TPANE*Q*

- FIGURE 7 A (v) -

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VGYEIMRAIKAPLAQIAINAGYDGGVVVNEVEKHEGHEGFNA
 M*IN*LR***ES*MR**VT***EAS***K*AE*KDNY***
 IKVALME***R**VL*C*EEPS**A*T*KGGD*NY*Y**
 I*AR*VLK*LS***K***A***KE*AIICQQ*LSRSSSE*YD*
 T*AN*VKV*LE***K***F*S*MEP***AEK*RNLSVGH*L**
 I*I***K*TL*I*AMT***K***V**SLI*EKIMQSSSEVGYD*

SNGKYVDMFKEGIIDPLKVERIALQNAVSVSSLLLTTEATVHEIK
 AT*E*G**VEM**L**T**T**M***A**A**M***CM*ADLP
 ATEE*GN*IDM**L**T**T**S***Y*A**AG*MI***CM*TDLP
 LRDA*T**IEA**L**T**T**C**ES*A**AG***LIAD*P
 AT*EYE*LL*A*VA**V**T**S***A*IAG*F***V*ADKP
 MA*DF*N*VEK***T**V**T**LD*A**A***T*A*VV**T**P

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EKAAPAMPDMGGMGMGMGMGM	HspB <i>Helicobacter pylori</i>
KKEEGVGAG*****	HtpB <i>Legionella pneumophila</i>
KND**--DLGAA*****	GroEL <i>Escherichia coli</i>
**SSSA-*A*P*A*--*DY	HypB <i>Chlamydia psittaci</i>
*KT***SDPTGGMGMDF	GroEL1 <i>Mycobacterium leprae</i>
D-*G*GA**--*M**G*F	63 kDa Human mitochondrial protein P1

Identity : 62.7%
 60.5%
 59.6%
 57.4%
 42.5%

Comparison of the GroEL-like proteins from various bacteria

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35%	<i>Helicobacter pylori</i>	MKFQPLGERVL
	<i>Mycobacterium leprae</i>	**EDKI*
35.6%	<i>Legionella pneumophila</i>	**IR**HD**V
33.8%	<i>Thermophilic bacterium</i>	*LK-***D*IV
32.2%	<i>Clostridium perfringens</i>	*SIK***D**V
20.3%	<i>Escherichia coli</i>	MNIR**HD**I

VERLEENKTSSGIIIPD	NAKEPLMGVVKAV---	SHKI
*QAG*A*TM*P**LV**ED*	***QE*T*V**GPGRWDE	
*R*M**RT*AG**V**S*T**MR*EI*	**GAGKVLE	
I*VV*T***A***VL**T***QE*R*V**GAGRVLD		
IK***A*ET*K***VTGT***R*QEAE*V**GPGAIVD		
*K*K*V*T*SAG**VLTGS*AA*STR*E*L**GNGRILE		

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SEGCKC---VKEGDVIAFGKYKGAEIVLDGVEYMVLELE
 DGAKRIPVD*S**IVIYS**G*T**KYN*E**LI*SAR
 NGDVRA---**V***VL***S*T*V*V**K*LV*MRED
 NGQRIGRKS-*V**RVI*S**A*T*VKY**K*Y*I*RES
 -GKRTEME-*I**KVLYS**A*T*VKFE*E**TI*RQD
 NGEVKP-LD**VG*IVI*NDGY*VKSEKIDN*EVLIMS*

DILGIVGSGSCCHTGNHDKHKAKEHEACCHDKKH
 *V*AV*SK
 **M*VIEK
 **AVIR
 ***A**E
 SDILAIVEA

Comparison of the GroES-like proteins from various bacteria

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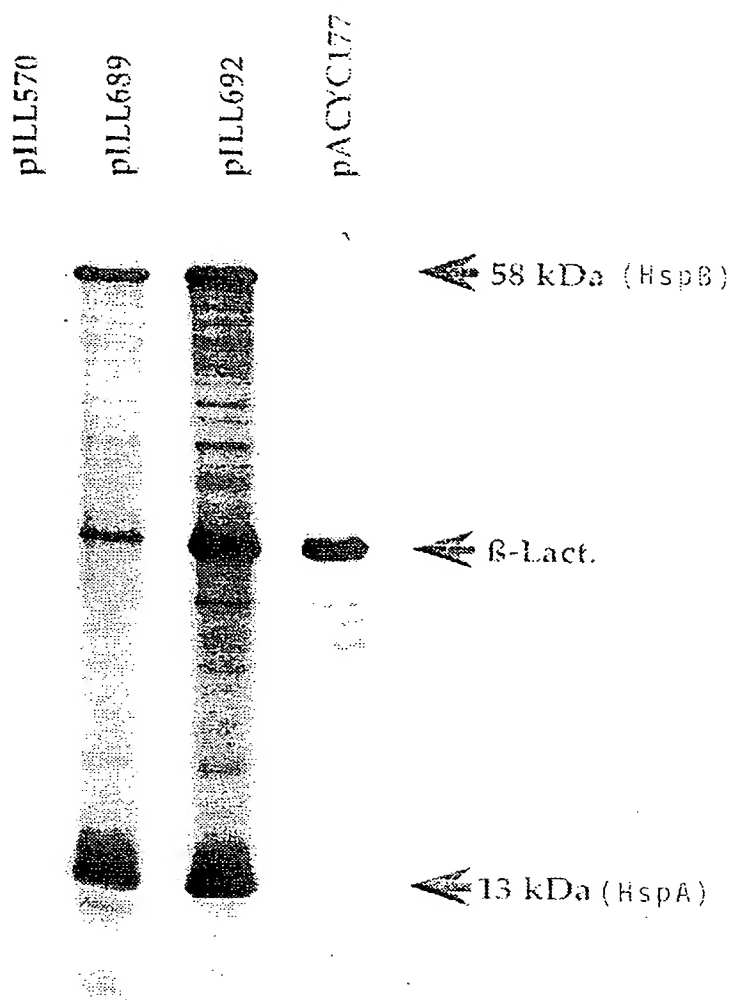


FIGURE 8

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1/1
ATG TTA GGT CTT GTG TTA TTG TAT GTT GCG
Met leu gly leu val leu leu tyr val ala

31/11
GTC GTG CTG ATC AGC AAC GGA GTT AGT GGG
val val leu ile ser asn gly val ser gly

- FIGURE 9 (i) -

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61/21

CTT GCA AAT GTG GAT GCC AAA AGC AAA GCC
leu ala asn val asp ala lys ser lys ala

91/31

ATC ATG AAC TAC TTT GTG GGG GGG GAC TCT
ile met asn tyr phe val gly gly asp ser

- FIGURE 9 (ii) -

121/41

CCA TTG TGT GTA ATG TGG TCG CTA TCA TCT
pro leu cys val met trp ser leu ser ser

151/51

TAT TCC ACT TTC CAC CCC ACC CCC CCT GCA
tyr ser thr phe his pro thr pro pro ala

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181/61

ACT GGT CCA GAA GAT GTC GCG CAG GTG TCT
thr gly pro glu asp val ala gln val ser

211/71

CAA CAC CTC ATT AAC TTC TAT GGT CCA GCG
gln his leu ile asn phe tyr gly pro ala

- FIGURE 9 (iv) -

241/81

ACT GGT CTA TTG TTT GGT TTT ACC TAC TTG
thr gly leu leu phe gly phe thr tyr leu

271/91

TAT GCT GCC ATC AAC AAC ACT TTC AAT CTC
tyr ala ala ile asn asn thr phe asn leu

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301/101
GAT TGG AAA CCC TAT GGC TGG TAT TGC TTG
asp trp lys pro tyr gly trp tyr cys leu

331/111
TTT GTA ACC ATC AAC ACT ATC CCA GCG GCC
phe val thr ile asn thr ile pro ala ala

361/121

ATT CTT TCT CAC TAT TCC GAT GCG CTT GAT
ile leu ser his tyr ser asp ala leu asp

391/131

GAT CAC CGC CTC TTA GGA ATC ACT GAG GGC
asp his arg leu leu gly ile thr glu gly

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421/141
GAT TGG TGG GCT TTC ATT TGG CTT GCT TGG
asp trp trp ala phe ile trp leu ala trp

451/151
GGT GTT TTG TGG CTC ACT GGT TGG ATT GAA
gly val leu trp leu thr gly trp ile glu

- FIGURE 9 (viii) -

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481/161
TGC GCA CTT GGT AAG AGT CTA GGT AAA TTT
cys ala leu gly lys ser leu gly lys phe

511/171
GTT CCA TGG CTT GCC ATC GTC GAG GGC GTG
val pro trp leu ala ile val glu gly val

- FIGURE 9 (ix) -

541/181
ATC ACC GCT TGG ATT CCT GCT TGG CTA CTC
ile thr ala trp ile pro ala trp leu leu

571/191
TTT ATC CAA CAC TGG TCT TGA
phe ile gln his trp ser OPA

The Genetic Code

		Second Position				
		U	C	A	G	
First Position (5' End)	U	UUU] Phe	UCU]	UAU] Tyr	UGU] Cys	U
		UUC]	UCC] Ser	UAC]	UGC]	C
		UUA] Leu	UCA]	UAA* Stop	UGA* Stop	A
		UUG]	UCG]	UAG* Stop	UGG Trp	G
	C	CUU]	CCU]	CAU] His	CGU]	U
		CUC] Leu	CCC]	CAC]	CGC] Arg	C
		CUA]	CCA]	CAA] Gln	CGA]	A
		CUG]	CCG]	CAG]	CGG]	G
	A	AUU]	ACU]	AAU] Asn	AGU] Ser	U
		AUC] Ile	ACC]	AAC]	AGC]	C
		AUA]	ACA]	AAA] Lys	AGA] Arg	A
		AUG* Met	ACG]	AAG]	AGG]	G
	G	GUU]	GCU]	GAU] Asp	GGU]	U
		GUC] Val	GCC]	GAC]	GGC]	C
		GUA]	GCA]	GAA] Glu	GGA]	A
		GUG*]	GCG]	GAG]	GGG]	G

Third Position (3' End)
- FIGURE 11 -

Abbreviations for amino acids

<i>Amino acid</i>	<i>Three-letter abbreviation</i>	<i>One-letter symbol</i>
Alanine	Ala	A
Arginine	Arg	R
Asparagine	Asn	N
Aspartic acid	Asp	D
Asparagine or aspartic acid	Asx	B
Cysteine	Cys	C
Glutamine	Gln	Q
Glutamic acid	Glu	E
Glutamine or glutamic acid	Glx	Z
Glycine	Gly	G
Histidine	His	H
Isoleucine	Ile	I
Leucine	Leu	L
Lysine	Lys	K
Methionine	Met	M
Phenylalanine	Phe	F
Proline	Pro	P
Serine	Ser	S
Threonine	Thr	T
Tryptophan	Trp	W
Tyrosine	Tyr	Y
Valine	Val	V

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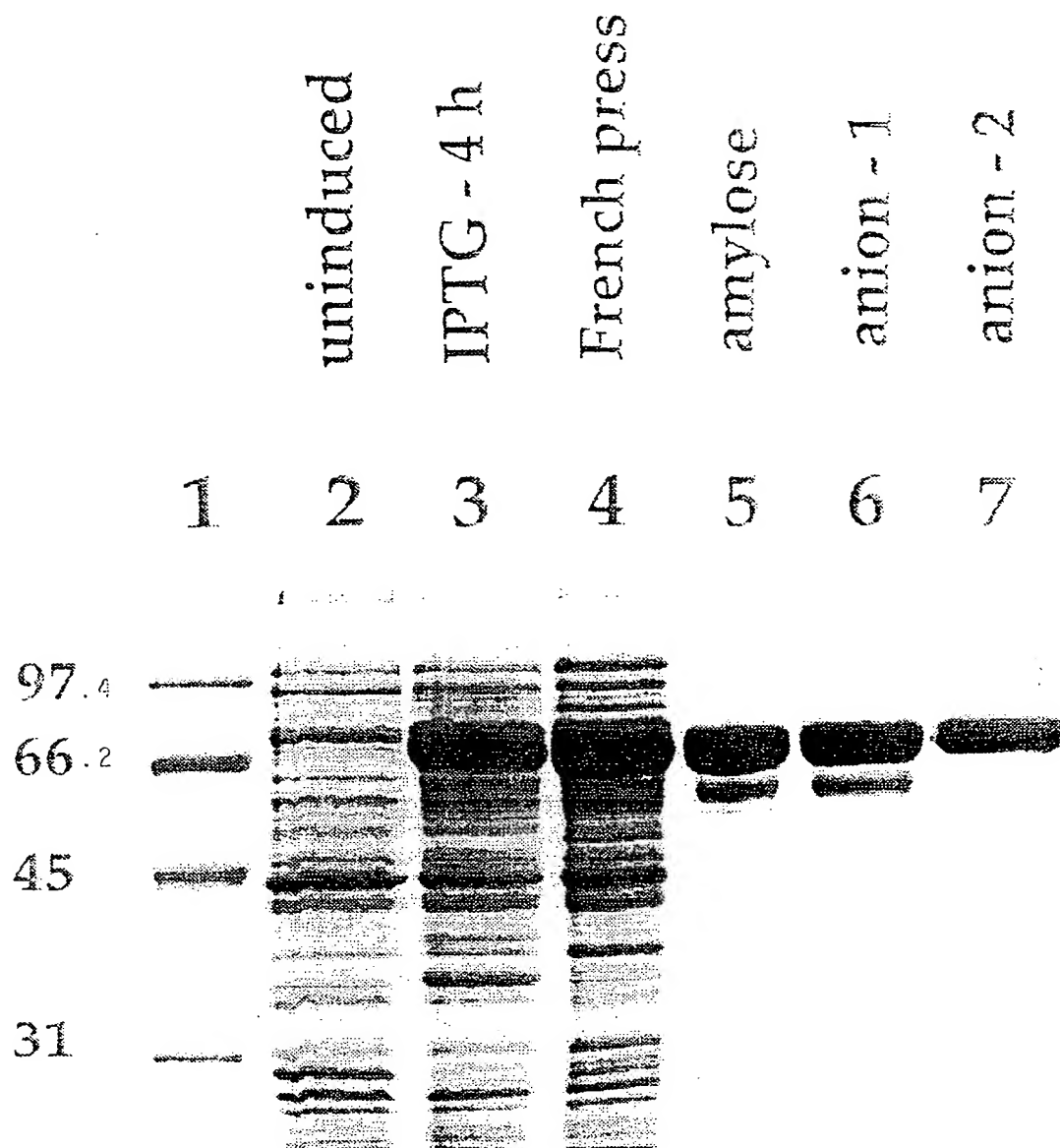
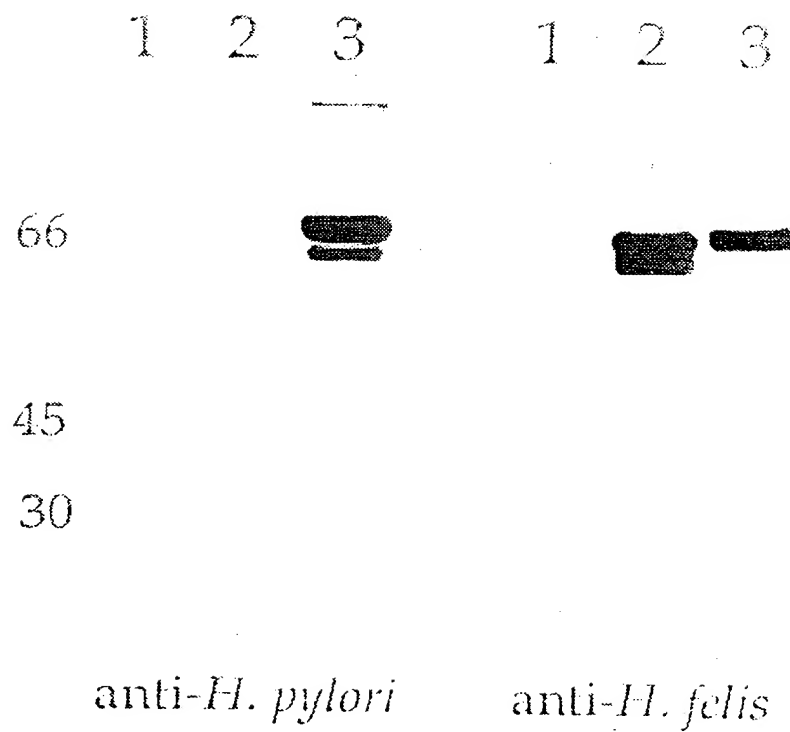


FIGURE 13

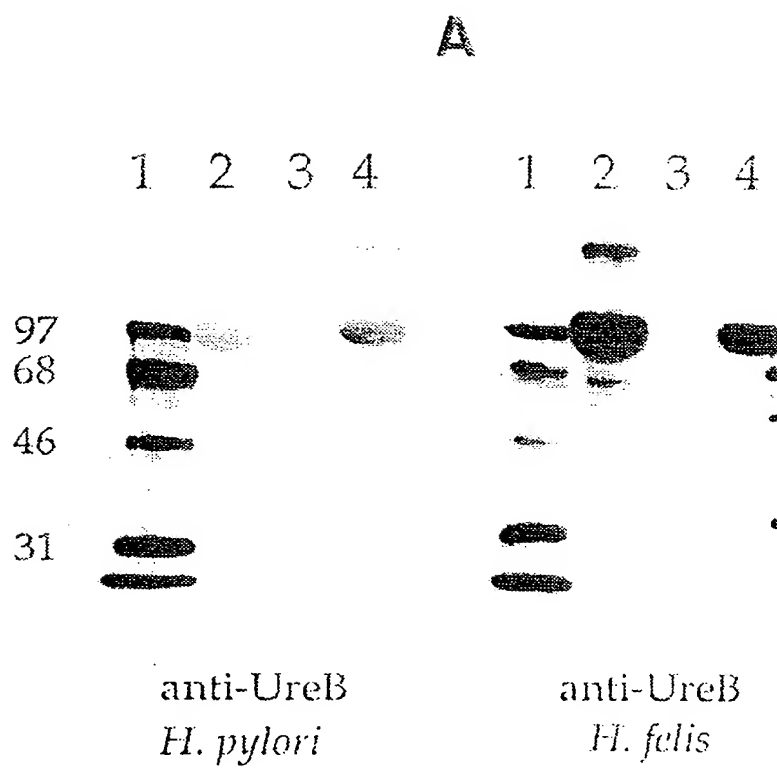
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FIGURE 14



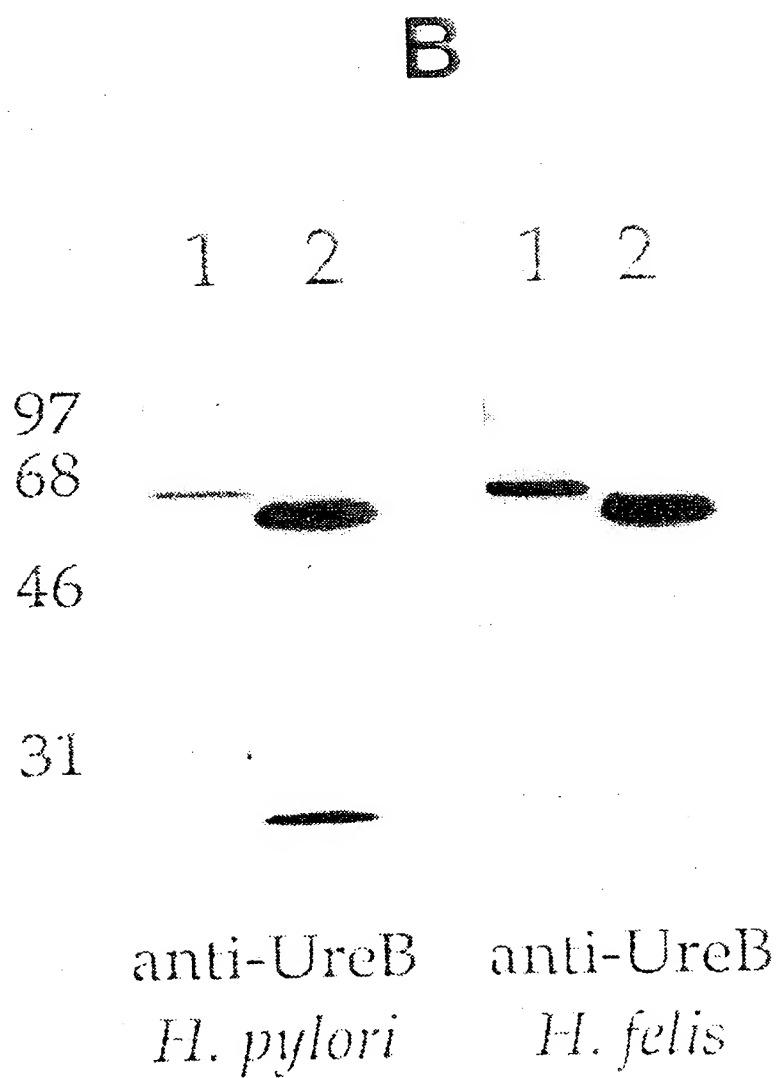
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FIGURE 15



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FIGURE 16.



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FIGURE 17(i)

HSP A - MBP FUSION

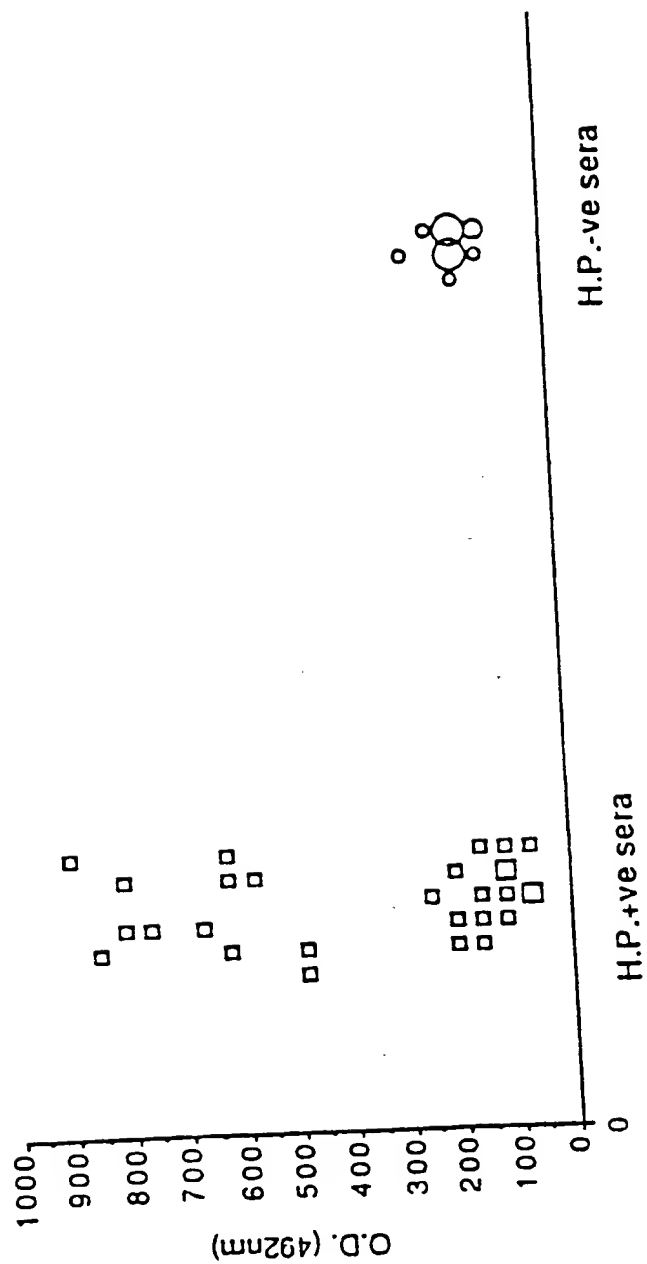
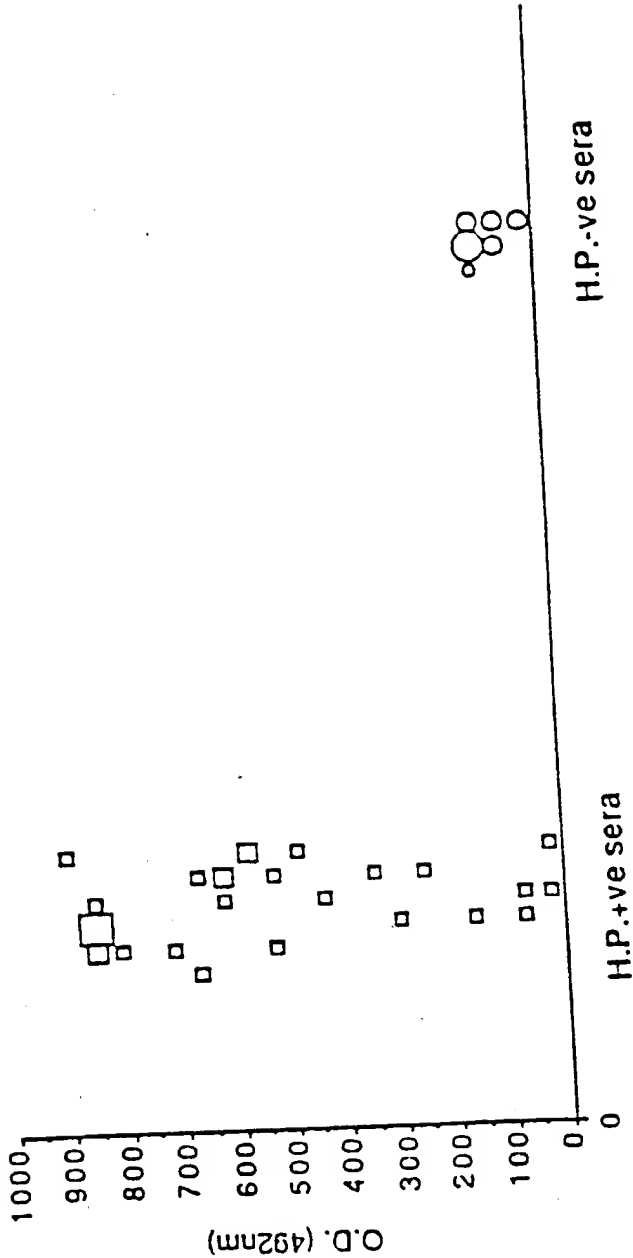


FIGURE 17(ii)

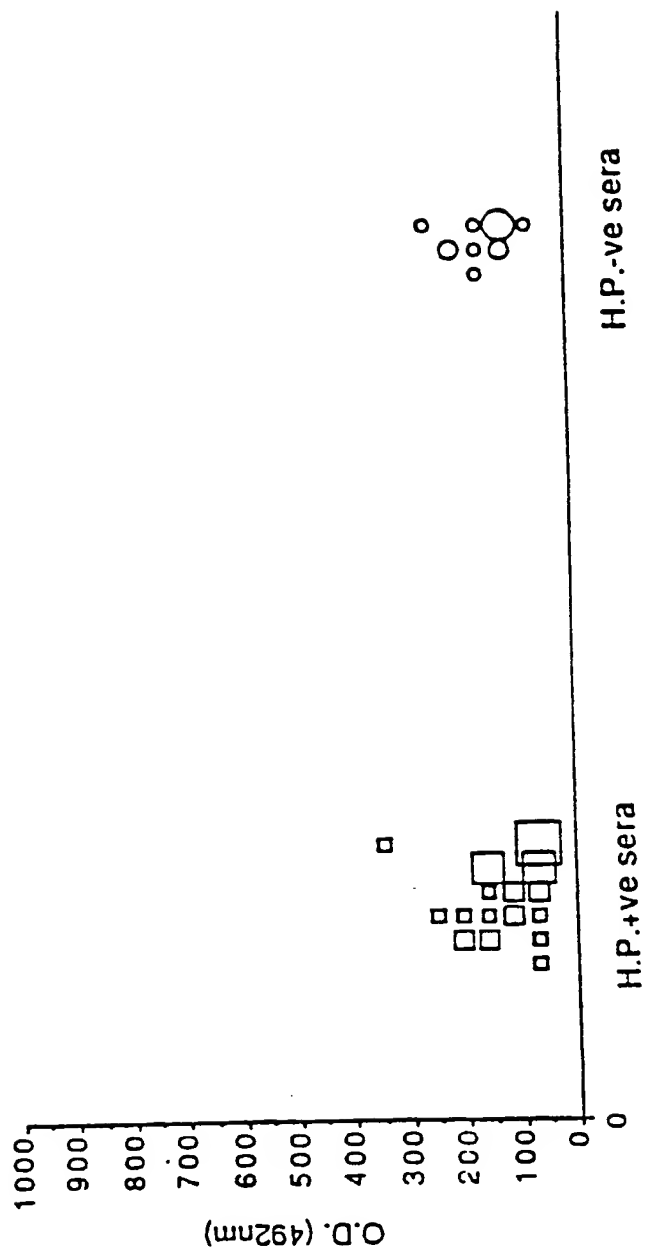
HSP B - MBP FUSION



55/56

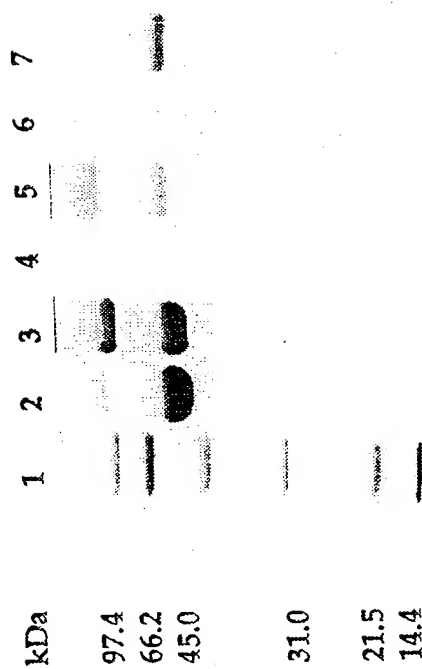
FIGURE 17(iii)

MBP



56/56

FIGURE 18



INTERNATIONAL SEARCH REPORT

Int'l Application No
PCT/EP 94/01625

A. CLASSIFICATION OF SUBJECT MATTER

IPC 5 : C12N15/31 C12N9/80 C12Q1/68 C12P21/08 A61K39/106
G01N33/577

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC 5 C12N C12Q C12P A61K G01N

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	GASTROENTEROLOGY, vol.104, no.4, April 1993, ELSEVIER, NEW YORK, U.S.;	10, 11, 20
Y	page A699 R.L. FERRERO ET AL. 'Molecular evidence demonstrating significant homology between the urease polypeptides of Helicobacter felis and Helicobacter pylori' Digestive disease week and the 94th annual meeting of the american gastroenterological association, May 15-21, 1993; Boston, Massachusetts, US;	7-9, 12-16, 22, 24-28, 31-35
	* page A699, left column, paragraph 2 * --- -/--	

☒ Further documents are listed in the continuation of box C.

☒ Patent family members are listed in annex.

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Date of the actual completion of the international search

10 October 1994

Date of mailing of the international search report

27. 10. 94

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C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	WO,A,93 07273 (INSTITUT PASTEUR) 15 April 1993 cited in the application * the whole document * ---	7-16,22, 24-28, 31-35
X	INFECTION AND IMMUNITY, vol.60, no.5, May 1992, AM. SOC. MICROBIOL., BALTIMORE, US; pages 1946 - 1951 B.E. DUNN ET AL. 'Identification and purification of a cpn60 heat shock protein homolog from Helicobacter pylori' cited in the application the whole document ---	17
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Y	WO,A,90 04030 (INSTITUT PASTEUR) 19 April 1990 the whole document ---	10-16, 20,21, 24,34,35
Y	WO,A,91 09049 (RESEARCH EXPLOITATION LIMITED) 27 June 1991 the whole document ---	10-16, 20,21, 24,34,35
Y	J. CLIN. MICROBIOL., vol.30, no.3, March 1992, AM. SOC. MICROBIOL., WASHINGTON, DC,US; pages 739 - 741 P.A. FOXALL ET AL. 'Use of polymerase chain reaction-amplified Helicobacter pylori urease structural genes for differentiation of isolates' the whole document ---	10-16, 20,21, 24,34,35
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P,Y	the whole document ---	34,35
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INTERNATIONAL SEARCH REPORT

Int'l Application No
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C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
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INTERNATIONAL SEARCH REPORT

Information on patent family members

Internat. Application No

PCT/EP 94/01625

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WO-A-9109049	27-06-91	NONE	
WO-A-9406474	31-03-94	AU-B- 4924893	12-04-94
WO-A-9318150	16-09-93	NONE	